

- (i) APPLICANTS: Reed, Steven G.
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- (ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
- (iii) NUMBER OF SEQUENCES: 153
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 13-MAR-1997
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.411C6
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG GTAGTTTGAA CCAAACGCAC AATCGACGGG CAAACGAACG GAAGAACACA 60
 ACCATGAAGA TGGTGAAATC GATCGCCGCA GGTCTGACCG CCGCGGCTGC AATCGGCGCC 120
 GCTGCGGCCG GTGTGACTTC GATCATGGCT GGCGGCCCGG TCGTATACCA GATGCAGCCG 180
 GTCGTCTTCG GCGCGCCACT GCCGTTGGAC CCGGCATCCG CCCCTGACGT CCCGACCGCC 240
 GCCCAGTTGA CCAGCCTGCT CAACAGCCTC GCCGATCCCA ACGTGTCGTT TGCGAACAAG 300
 GGCAGTCTGG TCGAGGGCGG CATCGGGGGC ACCGAGGCGC GCATCGCCGA CCACAAGCTG 360
 AAGAAGGCCG CCGAGCACGG GGATCTGCCG CTGTGTTCA GCGTGACGAA CATCCAGCCG 420
 GCGGCCGCCG GTTCGGCCAC CGCCGACGTT TCGTCTCGG GTCCGAAGCT CTCGTGCGCG 480
 GTCACGCAGA ACGTCACGTT CGTGAATCAA GGCGGCTGGA TGCTGTCACG CGCATCGGCG 540
 ATGGAGTTGC TGCAGGCCGC AGGGNAACTG ATTGGCGGGC CGGNTTCAGC CCGCTGTTCA 600
 GCTACGCCGC CCGCCTGGTG ACGCGTCCAT GTCGAACACT CGCGCGTGTA GCACGGTGCG 660
 GTNTGCGCAG GGNCGCACGC ACCGCCGGT GCAAGCCGTC CTCGAGATAG GTGGTGNCTC 720
 GNCACCAGNG ANCACCCCN NNTCGNCNNT TCTCGNTGNT GNATGA 766

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

09724633.1.2300

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC ACCATCACCA TCACACTTCT AACCGCCCAG CGCGTCGGGG GCGTCGAGCA	60
CCACGCGACA CCGGGCCCGA TCGATCTGCT AGCTTGAGTC TGGTCAGGCA TCGTCGTCAG	120
CAGCGCGATG CCCTATGTTT GTCGTGCACT CAGATATCGC GGCAATCCAA TCTCCCGCCT	180
GCGGCCGGCG GTGCTGCAAA CTACTCCCGG AGGAATTTCTG ACGTGCGCAT CAAGATCTTC	240
ATGCTGGTCA CGGCTGTCGT TTTGCTCTGT TGTTCGGGTG TGGCCACGGC CGCGCCCAAG	300
ACCTACTGCG AGGAGTTGAA AGGCACCGAT ACCGGCCAGG CGTGCCAGAT TCAAATGTCC	360
GACCCGGCCT ACAACATCAA CATCAGCCTG CCCAGTTACT ACCCCGACCA GAAGTCGCTG	420
GAAAATTACA TCGCCCAGAC GCGCGACAAG TTCCTCAGCG CGGCCACATC GTCCACTCCA	480
CGCGAAGCCC CCTACGAATT GAATATCACC TCGGCCACAT ACCAGTCCGC GATACCGCCG	540
CGTGGTACGC AGGCCGTGGT GCTCAMGGTC TACCACAACG CCGGCGGCAC GCACCCAACG	600
ACCACGTACA AGGCCTTCGA TTGGGACCAG GCCTATCGCA AGCCAATCAC CTATGACACG	660
CTGTGGCAGG CTGACACCGA TCCGCTGCCA GTCGTCTTCC CCATTGTTGC AAGGTGAACT	720
GAGCAACGCA GACCGGGACA ACWGGTATCG ATAGCCGCCN AATGCCGGCT TGGAACCCNG	780
TGAAATTATC ACAACTTCGC AGTCACNAAA NAA	813

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09724633.1.12000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC ACGGCCGCGT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTTCG	60
CATTCCGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC	120
CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTGACA ACAACGGCAA	180
CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC	240
CGGCGACGTG ATCACC GCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA	300
CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAAA CCAAGTCGGG	360
CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TCGTCGYGG	420
ATACCACCCG CCGGCCGGCC AATTGGA	447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC GGTGCGCGAG TATGTCGCCC AGCAAATGTC TGGCAGCCGC CCAACGGAAT	60
CCGGTGATCC GACGTCGAG GTTGTGCAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT	120
AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC	180
CCGGCGACGG NGAGCGCCGG AATGGCGCGA GTGAGCGGT GGNCAGTCAT GCCCAGNGG	240
ATCCAATCAA CCTGNATTCG GNCTGNNGGN CCATTTGACA ATCGAGGTAG TGAGCGCAAA	300
TGAATGATGG AAAACGGGNG GNGACGTCCG NTGTTCTGGT GGTGNTAGGT GNCTGNCTGG	360

NGTNGNGGNT ATCAGGATGT TCTTCGNCGA AANCTGATGN CGAGGAACAG GGTGTNCCCG	420
NNANNCCNAN GNGTCCNAN CCCNNNTCC TCGNCGANAT CANANAGNCG NTTGATGNGA	480
NAAAAGGGTG GANCAGNNNN AANTNGNGGN CCNAANAANC NNNANNGNNG NNAGNTNGNT	540
.NNNTNTTNNC ANNNNNNTG NNGNNGNNCN NNNCAANCNN NTNNNGNAA NNGGNTTNTT	600
NAAT	604

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCANGTCG AACCACCTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CGGTGGCGGC	60
CGCTCTAGAA CTAGTGKATM YYYCKGGCTG CAGSAATYCG GYACGAGCAT TAGGACAGTC	120
TAACGGTCCT GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA	180
CGGGTGCGAA CCCTCACCT CAACCGGCCG CAGTCCCGYA ACGCGCTCTC GGC GGCGCTA	240
CGGGATCGGT TTTTCGCGGY GTTGGYCGAC GCCGAGGYCG ACGACGACAT CGACGTCGTC	300
ATCCTCACCG GYGCCGATCC GGTGTTCTGC GCCGACTGG ACCTCAAGGT AGCTGGCCGG	360
GCAGACCGCG CTGCCGACA TCTACCGCG GTGGGCGGCC ATGACCAAGC CGGTGATCGG	420
CGCGATCAAC GGCGCCGCGG TCACCGCGG GCTCGAACTG GCGCTGTACT GCGACATCCT	480
GATCGCCTCC GAGCACGCC GCTTCGNCGA CACCCACGCC CGGGTGGGGC TGCTGCCAC	540
CTGGGGACTC AGTGTGTGCT TGCCGAAAA GGTCGGCATC GGNCTGGGCC GGTGGATGAG	600
CCTGACCGGC GACTACCTGT CCGTGACCGA CGC	633

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC	GGCGCCGGAG	AGCGGGCGCG	AACGGCGATC	GACGCGGCC	TGGCCAGAGT	60
CGGCACCACC	CAGGAGGGAG	TCGAATCATG	AAATTTGTCA	ACCATATTGA	GCCCGTCGCG	120
CCCCGCCGAG	CCGGCGGCGC	GGTCGCCGAG	GTCTATGCCG	AGGCCCCGCCG	CGAGTTCGGC	180
CGGCTGCCCCG	AGCCGCTCGC	CATGCTGTCC	CCGGACGAGG	GACTGCTCAC	CGCCGGCTGG	240
GCGACGTTGC	GCGAGACACT	GCTGGTGGGC	CAGGTGCCGC	GTGGCCGCAA	GGAAGCCGTC	300
GCCGCCGCCG	TCGCGGCCAG	CCTGCGCTGC	CCCTGGTGCG	TCGACGCACA	CACCACCATG	360
CTGTACGCGG	CAGGCCAAAC	CGACACCGCC	GCGGCGATCT	TGGCCGGCAC	AGCACCTGCC	420
GCCGGTGACC	CGAACGCGCC	GTATGTGGCG	TGGGCGGCAG	GAACCGGGAC	ACCGGCGGGA	480
CCGCCGGCAC	CGTTCGGCCC	GGATGTCGCC	GCCGAATACC	TGGGCACCGC	GGTGCAATTC	540
CACTTCATCG	CACGCCTGGT	CCTGGTGCTG	CTGGACGAAA	CCTTCCTGCC	GGGGGGCCCG	600
CGCGCCCAAC	AGCTCATGCG	CCGCGCCGGT	GGA CTGGTGT	TCGCCCGCAA	GGTGCGCGCG	660
GAGCATCGGC	CGGGCCGCTC	CACCCGCCGG	CTCGAGCCGC	GAACGCTGCC	CGACGATCTG	720
GCATCGGCAA	CACCGTCCGA	GCCCATAGCA	ACCGCGTTCG	CCGCGCTCAG	CCACCACCTG	780
GACACCGCGC	CGCACCTGCC	GCCACCGACT	CGTCAGGTGG	TCAGGCGGGT	CGTGGGGTCG	840
TGGCACGGCG	AGCCAATGCC	GATGAGCAGT	CGCTGGACGA	ACGAGCACAC	CGCCGAGCTG	900

CCCGCCGACC TGCACGCGCC CACCCGTCTT GCCCTGCTGA CCGGCCTGGC CCCGCATCAG 960
 GTGACCGACG ACGACGTCGC CGCGGCCCGA TCCCTGCTCG ACACCGATGC GGCCTGGTT 1020
 GCGGCCCTGG CCTGGGCCGC CTTACCGCC GCGCGGCGCA TCGGCACCTG GATCGGCGCC 1080
 GECGCCGAGG GCCAGGTGTC GCGGCAAAAC CCGACTGGGT GAGTGTGCGC GCCCTGTCGG 1140
 TAGGGTGTCA TCGCTGGCCC GAGGGATCTC GCGGCGGCGA ACGGAGGTGG CGACACAGGT 1200
 GGAAGCTGCG CCCACTGGCT TCGCCCCAA CGCGTCGTG GCGTTCGGT TGGCCGCACT 1260
 GGCCGATCAG GTCGGCGCCG GCCCTTGCC GAAGGTCCAG CTCAACGTGC CGTCACCGAA 1320
 GGACCGGACG GTCACCGGGG GTCACCCTGC GCGCCAAGG AA 1362

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGACCC CGATATGCCG GGCACCGTAG CGAAAGCCGT CGCCGACGCA CTCGGGCGCG 60
 GTATCGCTCC CGTTGAGGAC ATTCAGGACT GCGTGGAGGC CCGGCTGGGG GAAGCCGGTC 120
 TGGATGACGT GGCCCGTGTT TACATCATCT ACCGGCAGCG GCGCGCCGAG CTGCGGACGG 180
 CTAAGGCCTT GCTCGGCGTG CGGGACGAGT TAAAGCTGAG CTTGGCGGCC GTGACGGTAC 240
 TGC GCGAGCG CTATCTGCTG CACGACGAGC AGGGCCGGCC GGCCGAGTCG ACCGGCGAGC 300
 TGATGGACCG ATCGGCGCGC TGTGTCGCGG CGGCCGAGGA CCAGTATGAG CCGGGCTCGT 360
 CGAGGCGGTG GGCCGAGCGG TCGCCACGC TATTACGCAA CCTGGAATTC CTGCCGAATT 420
 CGCCCACGTT GATGAACTCT GGCACCGACC TGGGACTGCT CGCCGGCTGT TTGTTCTGC 480

CGATTGAGGA TTCGCTGCAA TCGATCTTTG CGACGCTGGG ACAGGCCCGCC GAGCTGCAGC 540
 GGGCTGGAGG CGGCACCGGA TATGCGTTCA GCCACCTGCG ACCCGCCGGG GATCGGGTGG 600
 CCTCCACGGG CGGCACGGCC AGCGGACCGG TGTCGTTTCT ACGGCTGTAT GACAGTGCCG 660
 CGGGTGTGGT CTCCATGGGC GGTGCGCCGGC GTGGCGCCTG TATGGCTGTG CTTGATGTGT 720
 CGCACCCGGA TATCTGTGAT TTCGTCACCG CCAAGGCCGA ATCCCCCAGC GAGCTCCCGC 780
 ATTTCAACCT ATCGGTTGGT GTGACCGACG CGTTCCTGCG GGCCGTCGAA CGCAACGGCC 840
 TACACCGGCT GGTCAATCCG CGAACCGGCA AGATCGTCGC GCGGATGCCC GCCGCCGAGC 900
 TGTTGACGC CATCTGCAA GCCGCGCACG CCGGTGGCGA TCCCGGGCTG GTGTTTCTCG 960
 ACACGATCAA TAGGGCAAAC CCGGTGCCGG GGAGAGGCCG CATCGAGGCG ACCAACCCGT 1020
 GCGGGGAGGT CCCACTGCTG CTTACGAGT CATGTAATCT CGGCTCGATC AACCTCGCCC 1080
 GGATGCTCGC CGACGGTCGC GTCGACTGGG ACCGGCTCGA GGAGGTCGCC GGTGTGGCGG 1140
 TGCGGTTCTT TGATGACGTC ATCGATGTCA GCCGCTACCC CTTCCCCGAA CTGGGTGAGG 1200
 CGGCCCCGCG CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTTGGCGGAA CTGCTTGCCG 1260
 CACTGGGTAT TCCGTACGAC AGTGAAGAAG CCGTGCGGTT AGCCACCCGG CTCATGCGTC 1320
 GCATACAGCA GGCGGCGCAC ACGGCATCGC GGAGGCTGGC CGAAGAGCGG GGCGCATTCC 1380
 CGGCGTTCAC CGATAGCCGG TTCGCGCGGT CGGGCCCGAG GCGCAACGCA CAGGTCACCT 1440
 CCGTCGCTCC GACGGGCA 1458

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAA	CGTGCTGGAT	CTGGAACCGC	GTGGCCCGCT	ACCTACCGAG	ATCTACTGGC	60
GGCGCAGGGG	GCTGGCCCTG	GGCATCGCGG	TCGTCGTAGT	CGGGATCGCG	GTGGCCATCG	120
TCATCGCCTT	CGTCGACAGC	AGCGCCGGTG	CCAAACCGGT	CAGCGCCGAC	AAGCCGGCCT	180
CCGCCCAGAG	CCATCCGGGC	TCGCCGGCAC	CCCAAGCACC	CCAGCCGGCC	GGGCAAACCG	240
AAGGTAACGC	CGCCGCGGCC	CCGCCGCAGG	GCCAAAACCC	CGAGACACCC	ACGCCCACCG	300
CCGCGGTGCA	GCCGCCGCCG	GTGCTCAAGG	AAGGGGACGA	TTGCCCCGAT	TCGACGCTGG	360
CCGTCAAAGG	TTTGACCAAC	GCGCCGCAGT	ACTACGTCGG	CGACCAGCCG	AAGTTCACCA	420
TGGTGGTCAC	CAACATCGGC	CTGGTGTCTT	GTAAACGCGA	CGTTGGGGCC	GCGGTGTTGG	480
CCGCCTACGT	TTACTCGCTG	GACAACAAGC	GGTTGTGGTC	CAACCTGGAC	TGCGCGCCCT	540
CGAATGAGAC	GCTGGTCAAG	ACGTTTTCCC	CCGGTGAGCA	GGTAACGACC	GCGGTGACCT	600
GGACCGGGAT	GGGATCGGCG	CCGCGCTGCC	CATTGCCGCG	GCCGGCGATC	GGGCCGGGCA	660
CCTACAATCT	CGTGGTACAA	CTGGGCAATC	TGCGCTCGCT	GCCGGTTCCG	TTCATCCTGA	720
ATCAGCCGCC	GCCGCCGCC	GGGCCGGTAC	CCGCTCCGGG	TCCAGCGCAG	GCGCCTCCGC	780
CGGAGTCTCC	CGCGCAAGGC	GGATAATTAT	TGATCGCTGA	TGGTCGATTC	CGCCAGCTGT	840
GACAACCCCT	CGCCTCGTGC	CG				862

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC CAATGACAAA 60
 GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGCTGCCGC GAACGCTGGA 120
 GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG CGCGGACGCG 180
 TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GGCGCCACGG TGGCGCTAAC CTTTCAGGAT 240
 CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA GTGATGAAGG 300
 TCGCCGCGCA GTGTTCAAAG CTCGGATATA CGGTGGCACC CATGGAACAG CGTGCGGAGT 360
 TGGTGGTTGG CCGGGCACTT GTCGTCGTCG TTGACGATCG CACGGCGCAC GGCGATGAAG 420
 ACCACAGCGG GCCGCTTGTC ACCGAGCTGC TCACCGAGGC CGGGTTTGTT GTCGACGGCG 480
 TGGTGGCGGT GTCGGCCGAC GAGGTCGAGA TCCGAAATGC GCTGAACACA GCGGTGATCG 540
 GCGGGGTGGA CCTGGTGGTG TCGGTCGGCG GGACCGNGT GACGNCTCGC GATGTCACCC 600
 CGGAAGCCAC CCGNGACATT CT 622

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGCAGCGG TAAGCCTGTT GGCCGCCGGC AACTGGTGT TGACAGCATG CGGCGGTGGC 60
 ACCAACAGCT CGTCGTCAGG CGCAGGCGGA ACGTCTGGGT CGGTGCACTG CGGCGGCAAG 120
 AAGGAGCTCC ACTCCAGCGG CTCGACCGCA CAAGAAAATG CCATGGAGCA GTTCGTCTAT 180

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GCCTACGTGC GATCGTGCCC GGGCTACACG TTGGACTACA ACGCCAACGG GTCCGGTGCC 240
 GGGGTGACCC AGTTTCTCAA CAACGAAACC GATTTGCGCG GCTCGGATGT CCCGTTGAAT 300
 CCGTCGACCG GTCAACCTGA CCGGTCGGCG GAGCGGTGCG GTTCCCCGGC ATGGGACCTG 360
 CCGACGGTGT TCGGCCCGAT CGCGATCACC TACAATATCA AGGGCGTGAG CACGCTGAAT 420
 CTTGACGGAC CCACTACCGC CAAGATTTTC AACGGCACCA TCACCGGTG GAATGATCCA 480
 CAGATCCAAG CCCTCAACTC CGGCACCGAC CTGCCGCCAA CACCGATTAG CGTTATCTTC 540
 CGCAGCGACA AGTCCGGTAC GTCGGACAAC TTCCAGAAAT ACCTCGACGG TGTATCCAAC 600
 GGGGCGTGGG GCAAAGGCGC CAGCGAAACG TTCAGCGGGG GCGTCGGCGT CGGCGCCAGC 660
 GGAACAACG GAACGTCGGC CCTACTGCAG ACGACCGACG GGTGATCAC CTACAACGAG 720
 TGGTCGTTTG CCGTGGGTAA GCAGTTGAAC ATGGCCCAGA TCATCACGTC GGCGGGTCCG 780
 GATCCAGTGG CGATCACCAC CGAGTCGGTC GGTAAGACAA TCGCCGGGGC CAAGATCATG 840
 GGACAAGGCA ACGACCTGGT ATTGGACACG TCGTCGTTCT ACAGACCCAC CCAGCCTGGC 900
 TCTTACCCGA TCGTGCTGGC GACCTATGAG ATCGTCTGCT CGAAATACCC GGATGCGACG 960
 ACCGGTACTG CGGTAAGGGC GTTTATGCAA GCCGCGATTG GTCCAGGCCA AGAAGGCCTG 1020
 GACCAATACG GCTCCATTCC GTTGCCCAA TCGTTCCAAG CAAAATTGGC GGCCGCGGTG 1080
 AATGCTATTT CTTGACCTAG TGAAGGGAAT TCGACGGTGA GCGATGCCGT TCCGCAGGTA 1140
 GGGTCGCAAT TTGGGCCGTA TCAGCTATTG CGGCTGCTGG GCCGAGGCGG GATGGGCGAG 1200

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCCGTC TGGTGTTTGA ACGGTTTTAC CGGTCGGCAT CGGCACGGGC GTTGCCGGGT	60
TCGGGCCTCG GGTTGGCGAT CGTCAAACAG GTGGTGCTCA ACCACGGCGG ATTGCTGCGC	120
ATCGAAGACA CCGACCCAGG CGGCCAGCCC CCTGGAACGT CGATTACGT GCTGCTCCCC	180
GGCCGTCGGA TGCCGATTCC GCAGCTTCCC GGTGCGACGG CTGGCGCTCG GAGCACGGAC	240
ATCGAGAACT CTCGGGGTTC GCGAACGTT ATCTCAGTGG AATCTCAGTC CACGCGCGCA	300
ACCTAGTTGT GCAGTTACTG TTGAAAGCCA CACCCATGCC AGTCCACGCA TGGCCAAGTT	360
GGCCCGAGTA GTGGGCCTAG TACAGGAAGA GCAACCTAGC GACATGACGA ATCACCCACG	420
GTATTGCGCA CCGCCGCAGC AGCCGGGAAC CCCAGGTTAT GCTCAGGGGC AGCAGCAAAC	480
GTACAGCCAG CAGTTCGACT GGC GTTACCC ACCGTCCCCG CCCCCGCAGC CAACCCAGTA	540
CCGTCAACCC TACGAGGCGT TGGGTGGTAC CCGGCCGGGT CTGATACCTG GCGTGATTCC	600
GACCATGACG CCCCCTCCTG GGATGGTTCG CCAACGCCCT CGTGCAGGCA TGTTGGCCAT	660
CGGCGCGGTG ACGATAGCGG TGGTGTCCGC CGGCATCGGC GGC GCGGCCG CATCCCTGGT	720
CGGGTTCAAC CGGGCACCCG CCGGCCCCAG CGGCGGCCCA GTGGCTGCCA GCGCGGCGCC	780
AAGCATCCCC GCAGCAAACA TGCCGCCGGG GTCGGTCGAA CAGGTGGCGG CCAAGGTGGT	840
GCCAGTGTC GTCATGTTGG AAACCGATCT GGGCCGCCAG TCGGAGGAGG GCTCCGGCAT	900
CATTCTGTCT GCCGAGGGGC TGATCTTGAC CAACAACCAC GTGATCGCGG CGGCCGCCAA	960

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GCCTCCCCTG GGCAGTCCGC CGCCGAAAAC GACGGTAACC TTCTCTGACG GGC GGACCGC 1020
 ACCCTTCACG GTGGTGGGGG CTGACCCAC CAGTGATATC GCCGTCGTCC GTGTTCAGGG 1080
 CGTCTCCGGG CTCACCCCGA TCTCCCTGGG TTCCTCCTCG GACCTGAGGG TCGGTCAGCC 1140
 GGTGCTGGCG ATCGGGTCGC CGCTCGGTTT GGAGGGCACC GTGACCACGG GGATCGTCAG 1200
 CGCTCTCAAC CGTCCAGTGT CGACGACCGG CGAGGCCGGC AACCAGAACA CCGTGCTGGA 1260
 CGCCATTCAG ACCGACGCCG CGATCAACCC CGGTA ACTCC GGGGGCGCGC TGGTGAACAT 1320
 GAACGCTCAA CTCGTCGGAG TCAACTCGGC CATTGCCACG CTGGGCGCGG ACTCAGCCGA 1380
 TGC GCAGAGC GGCTCGATCG GTCTCGGTTT TGC GATTCCA GTCGACCAGG CCAAGCGCAT 1440
 CGCCGACGAG TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC 1500
 CAATGACAAA GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGCTGCCGC 1560
 GAACGCTGGA GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG 1620
 CGCGGACGCG TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GGC GCCACGG TGGCGCTAAC 1680
 CTTTCAGGAT CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA 1740
 GTGATGAAGG TCGCCGCGCA GTGTTCAAAG C 1771

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGCG GTGGCGGCCG CTCTAGAACT AGTGGATCCC CCGGGCTGCA GGAATTCGGC 60
 ACGAGGATCC GACGTCGCAG GTTGTGCAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT 120

AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC 180
 CCGGCGACGG CGAGCGCCGG AATGGCGCGA GTGAGGAGGC GGGCAGTCAT GCCCAGCGTG 240
 ATCCAATCAA CCTGCATTCG GCCTGCGGGC CCATTTGACA ATCGAGGTAG TGAGCGCAAA 300
 TGAATGATGG AAAACGGGCG GTGACGTCCG CTGTTCTGGT GGTGCTAGGT GCCTGCCTGG 360
 CGTTGTGGCT ATCAGGATGT TCTTCGCCGA AACCTGATGC CGAGGAACAG GGTGTTCCCG 420
 TGAGCCCGAC GGCGTCCGAC CCCGCGCTCC TCGCCGAGAT CAGGCAGTCG CTTGATGCGA 480
 CAAAAGGGTT GACCAGCGTG CACGTAGCGG TCCGAACAAC CGGGAAAGTC GACAGCTTGC 540
 TGGGTATTAC CAGTGCCGAT GTCGACGTCC GGGCCAATCC GCTCGCGGCA AAGGGCGTAT 600
 GCACCTACAA CGACGAGCAG GGTGTCCCGT TTCGGGTACA AGGCGACAAC ATCTCGGTGA 660
 AACTGTTCGA CGACTGGAGC AATCTCGGCT CGATTTCTGA ACTGTCAACT TCACGCGTGC 720
 TCGATCCTGC CGCTGGGGTG ACGCAGCTGC TGTCCGGTGT CACGAACCTC CAAGCGCAAG 780
 GTACCGAAGT GATAGACGGA ATTTGACCA CAAAATCAC CGGGACCATC CCCGCGAGCT 840
 CTGTCAAGAT GCTTGATCCT GGCGCCAAGA GTGCAAGGCC GGCGACCGTG TGGATTGCCC 900
 AGGACGGCTC GCACCACCTC GTCCGAGCGA GCATCGACCT CGGATCCGGG TCGATTCAGC 960
 TCACGCAGTC GAAATGGAAC GAACCCGTCA ACGTCGACTA GGCCGAAGTT GCGTCGACGC 1020
 GTTGNTCGAA ACGCCCTTGT GAACGGTGTC AACGGNAC 1058

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGAGAGGTGA TCGACATCAT CGGGACCAGC CCCACATCCT GGGAACAGGC	60
GGCGGCGGAG GCGGTCCAGC GGGCGCGGGA TAGCGTCGAT GACATCCGCG TCGCTCGGGT	120
CATTGAGCAG GACATGGCCG TGGACAGCGC CGGCAAGATC ACCTACCGCA TCAAGCTCGA	180
AGTGTCGTTC AAGATGAGGC CGGCGCAACC GCGCTAGCAC GGGCCGGCGA GCAAGACGCA	240
AAATCGCACG GTTTGCGGTT GATTCGTGCG ATTTTGTGTC TGCTCGCCGA GGCCTACCAG	300
GCGCGGCCCA GGTCCGCGTG CTGCCGTATC CAGGCGTGCA TCGCGATTCC GCGGGCCACG	360
CCGGAGTTAA TGC.TTCGCGT CGACCCGAAC TGGGCGATCC GCCGGNGAGC TGATCGATGA	420
CCGTGGCCAG CCCGTCGATG CCCGAGTTGC CCGAGGAAAC GTGCTGCCAG GCCGGTAGGA	480
AGCGTCCGTA GCGGGCGGTG CTGACCGGCT CTGCCTGCGC CCTCAGTGCG GCCAGCGAGC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCCGCC CGCGCCTCCG TTGCCCCCAT TGCCGCCGTC GCCGATCAGC TGCGCATCGC	60
CACCATCACC GCCTTTGCCG CCGGCACCGC CGGTGGCGCC GGGGCCGCCG ATGCCACCGC	120
TTGACCCTGG CCGCCGGCGC CGCCATTGCC ATACAGCACC CCGCCGGGGG CACCGTTACC	180
GCCGTCGCCA CCGTCGCCGC CGCTGCCGTT TCAGGCCGGG GAGGCCGAAT GAACCGCCGC	240
CAAGCCCGCC GCCGGCACCG TTGCCGCCTT TTCCGCCCGC CCGCCGGCG CCGCCAATTG	300

00724600 412000

CCGAACAGCC AMGCACCGTT GCCGCCAGCC CCGCCGCCGT TAACGGCGCT GCCGGGCGCC 360
 GCCGCCGGAC CCGCCATTAC CGCCGTTCCC GTTCGGTGCC CCGCCGTTAC CGGCGCCGCC 420
 GTTTGCCGCC AATATTCGGC GGGCACCGCC AGACCCGCCG GGGCCACCAT TGCCGCCGGG 480
 CACCGAAACA ACAGCCCAAC GGTGCCGCCG GCCCCGCCGT TTGCCGCCAT CACCGGCCAT 540
 TCACCGCCAG CACCGCCGTT AATGTTTATG AACCCGGTAC CGCCAGCGCG GCCCCTATTG 600
 CCGGGCGCCG GAGNGCGTGC CCGCCGGCGC CGCCAACGCC CAAAAGCCCG GGGTTGCCAC 660
 CGGCCCCGCC GGACCCACCG GTCCCGCCGA TCCCCCGTT GCCGCCGGTG CCGCCGCCAT 720
 TGGTGCTGCT GAAGCCGTTA GCGCCGGTTC CGCSGGTTCC GGCGGTGGCG CCNTGGCCGC 780
 CGGCCCCGCC GTTGCCGTAC AGCCACCCCC CGGTGGCGCC GTTGCCGCCA TTGCCGCCAT 840
 TGCCGCCGTT GCCGCCATTG CCGCCGTTCC CGCCGCCACC GCCGGNTTGG CCGCCGGCGC 900
 CGCCGGCGGC CGC 913

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG GTGTAGAAAA ATCCTGCCGC CCGGACCCTT AAGGCTGGGA CAATTTCTGA 60
 TAGCTACCCC GACACAGGAG GTTACGGGAT GAGCAATTCG CGCCGCCGCT CACTCAGGTG 120
 GTCATGGTTG CTGAGCGTGC TGGCTGCCGT CGGGCTGGGC CTGGCCACGG CGCCGGCCCA 180
 GGCGGCCCCG CCGGCCTTGT CGCAGGACCG GTTCGCCGAC TTCCCCGCGC TGCCCTCGA 240

002403W 442000

CCCGTCCGCG ATGGTCGCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAACCTGGG 300
 CTACAACAAC GCCGTGGGCG CCGGGACCGG CATCGTCATC GATCCCAACG GTGTCGTGCT 360
 GACCAACAAC CACGTGATCG CGGGCGCCAC CGACATCAAT GCGTTCAGCG TCGGCTCCGG 420
 CCAAACCTAC GGCCTCGATG TGGTCGGGTA TGACCGCACC CAGGATGTCT CGGTGCTGCA 480
 GCTGCGCGGT GCCGGTGGCC TGCCGTCGGC GGCGATCGGT GGCGGCGTCG CGGTTGGTGA 540
 GCCCGTCGTC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACGCCCCGTG CGGTGCCTGG 600
 CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GCGTTCGGAT TCGCTGACCG GTGCCGAAGA 660
 GACATTGAAC GGGTTGATCC AGTTCGATGC CGCAATCCAG CCCGGTGATT CGGGCGGGCC 720
 CGTCGTCAAC GGCCTAGGAC AGGTGGTCGG TATGAACACG GCCGCGTCCG ATAACCTCCA 780
 GCTGTCCCAG GGTGGGCAGG GATTCGCCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG 840
 CCAAATCCGA TCGGGTGGGG GGTCACCCAC CGTTCATATC GGGCCTACCG CCTTCCTCGG 900
 CTTGGGTGTT GTCGACAACA ACGGCAACGG CGCACGAGTC CAACGCGTGG TCGGAAGCGC 960
 TCCGGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC ACCGCGGTCTG ACGGCGCTCC 1020
 GATCAACTCG GCCACCGCGA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCAT 1080
 CTCGGTGAAC TGGCAAACCA AGTCGGGCGG CACGCGTACA GGGAACGTGA CATTGGCCGA 1140
 GGGACCCCCG GCCTGATTTG TCGCGGATAC CACCCGCCGG CCGGCCAATT GGATTGGCGC 1200
 CAGCCGTGAT TGCCGCGTGA GCCCCGAGT TCCGTCTCCC GTGCGCGTGG CATTGTGGAA 1260
 GCAATGAACG AGGCAGAACA CAGCGTTGAG CACCCTCCCG TGCAGGGCAG TTACGTCGAA 1320
 GGCGGTGTGG TCGAGCATCC GGATGCCAAG GACTTCGGCA GCGCCGCCGC CCTGCCCGCC 1380
 GATCCGACCT GGTTTAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC 1440
 GCCAGCGCGG ACGGTTCCGN CGATCTGCGT GGAATCATCG ATCGCCTCGA CTACCTGCAG 1500
 TGGCTTGGCA TCGACTGCAT CTGTTGCCGC CGTTCCTACG ACTACCGCT GCGCGACGGC 1560
 GGTTACGACA TTCGCGACTT CTACAAGGTG CTGCCCGAAT TCGGCACCGT CGACGATTC 1620

00724633.42300

(2) INFORMATION FOR SEQ ID NO:18:

(A) LENGTH: 1482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

CTTCGCCGAA	ACCTGATGCC	GAGGAACAGG	GTGTTCCCGT	GAGCCCGACG	GCGTCCGACC	60
CCGCGCTCCT	CGCCGAGATC	AGGCAGTCGC	TTGATGCGAC	AAAAGGGTTG	ACCAGCGTGC	120
ACGTAGCGGT	CCGAACAACC	GGGAAAGTCG	ACAGCTTGCT	GGGTATTACC	AGTGCCGATG	180
TCGACGTCCG	GGCCAATCCG	CTCGCGGCAA	AGGGCGTATG	CACCTACAAC	GACGAGCAGG	240
GTGTCCCGTT	TCGGGTACAA	GGCGACAACA	TCTCGGTGAA	ACTGTTCGAC	GA CTGGAGCA	300
ATCTCGGCTC	GATTTCTGAA	CTGTCAACTT	CACGCGTGCT	CGATCCTGCC	GCTGGGGTGA	360
CGCAGCTGCT	GTCCGGTGTC	ACGAACCTCC	AAGCGCAAGG	TACCGAAGTG	ATAGACGGAA	420
TTTCGACCAC	CAAAATCACC	GGGACCATCC	CCGCGAGCTC	TGTCAAGATG	CTTGATCCTG	480
GCGCCAAGAG	TGCAAGGCCG	GCGACCGTGT	GGATTGCCCA	GGACGGCTCG	CACCACCTCG	540
TCCGAGCGAG	CATCGACCTC	GGATCCGGGT	CGATTCAGCT	CACGCAGTCG	AAATGGAACG	600

AACCCGTCAA CGTCGACTAG GCCGAAGTTG CGTCGACGCG TTGCTCGAAA CGCCCTTGTG 660
 AACGGTGTCA ACGGCACCCG AAAACTGACC CCCTGACGGC ATCTGAAAAT TGACCCCTA 720
 GACCGGGCGG TTGGTGGTTA TTCTTCGGTG GTTCCGGCTG GTGGGACGCG GCCGAGGTG 780
 CGGTCTTTGA GCCGGTAGCT GTCGCCTTTG AGGGCGACGA CTTCAGCATG GTGGACGAGG 840
 CGGTCGATCA TGGCGGCAGC AACGACGTCG TCGCCGCCGA AACCTCGCC CCACCGGCCG 900
 AAGGCCTTAT TGGACGTGAC GATCAAGCTG GCCCGCTCAT ACCGGGAGGA CACCAGCTGG 960
 AAGAAGAGGT TGGCGGCCTC GGGCTCAAAC GGAATGTAAC CGACTTCGTC AACCACCAGG 1020
 AGCGGATAGC GGCCAAACCG GGTGAGTTCG GCGTAGATGC GCCCGGCGTG GTGAGCCTCG 1080
 GCGAACCGTG CTACCCATTC GGCGGCGGTG GCGAACAGCA CCCGATGACC GGCCTGACAC 1140
 GCGCGTATCG CCAGGCCGAC CGCAAGATGA GTCTTCCCGG TGCCAGGCGG GGCCCAAAAA 1200
 CACGACGTTA TCGCGGGCGG TGATGAAATC CAGGGTGCCC AGATGTGCGA TGGTGTCGCG 1260
 TTTGAGGCCA CGAGCATGCT CAAAGTCGAA CTCTTCCAAC GACTTCCGAA CCGGGAAGCG 1320
 GGCGGCGCGG ATGCGGCCCT CACCACCATG GGA CTCCCGG GCTGACACTT CCCGCTGCAG 1380
 GCAGGCGGCC AGGTATTCTT CGTGGCTCCA GTTCTCGGCG CGGGCGCGAT CGGCCAGCCG 1440
 GGACACTGAC TCACGCAGGG TGGGAGCTTT CAATGCTCTT GT 1482

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA CGAGCCGGCG ATAGCTTCTG GGCCGCGGCC GACCAGATGG CTCGAGGGTT 60

(2) INFORMATION FOR SEQ ID NO:20:

(A) LENGTH: 1021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATCCCCCGG GCTGCAGGAA TTCGGCACGA GAGACAAAT TCCACGCGTT AATGCAGGAA 60

CAGATTCATA ACGAATTCAC AGCGGCACAA CAATATGTCG CGATCGCGGT TTATTTTCGAC 120
 AGCGAAGACC TGCCGCAGTT GGCGAAGCAT TTTTACAGCC AAGCGGTCGA GGAACGAAAC 180
 CATGCAATGA TGCTCGTGCA ACACCTGCTC GACCGCGACC TTCGTGTCGA AATTCCCGGC 240
 GTAGACACGG TGC GAAACCA GTTCGACAGA CCCC GCGAGG CACTGGCGCT GGC GCTCGAT 300
 CAGGAACGCA CAGTCACCGA CCAGGTCGGT CGGCTGACAG CGGTGGCCCG CGACGAGGGC 360
 GATTTCTCTG GCGAGCAGTT CATGCAGTGG TTCTTG CAGG AACAGATCGA AGAGGTGGCC 420
 TTGATGGCAA CCCTGGTGCG GGTTGCCGAT CGGGCCGGGG CCAACCTGTT CGAGCTAGAG 480
 AACTTCGTCG CACGTGAAGT GGATGTGGCG CCGGCCGCAT CAGGCGCCCC GCACGCTGCC 540
 GGGGGCCGCC TCTAGATCCC TGGGGGGGAT CAGCGAGTGG TCCCGTTCGC CCGCCCGTCT 600
 TCCAGCCAGG CCTTGGTGCG GCCGGGGTGG TGAGTACCAA TCCAGGCCAC CCCGACCTCC 660
 CGGNAAAAGT CGATGTCCTC GTACTCATCG ACGTTCCAGG AGTACACCGC CCGGCCCTGA 720
 GCTGCCGAGC GGTCAACGAG TTGCGGATAT TCCTTTAACG CAGGCAGTGA GGGTCCCACG 780
 GCGGTTGGCC CGACCGCCGT GGCCGCACTG CTGGTCAGGT ATCGGGGGGT CTTGGCGAGC 840
 AACACGTCG GCAGGAGGGG TGGAGCCCGC CGGATCCGCA GACCGGGGGG GCGAAAACGA 900
 CATCAACACC GCACGGGATC GATCTGCGGA GGGGGGTGCG GGAATACCGA ACCGGTGTAG 960
 GAGCGCCAGC AGTTGTTTTT CCACCAGCGA AGCGTTTTTCG GGTCATCGGN GGCNNTTAAG 1020
 T 1021

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGACG AACGGAAGAA CACAACCATG AAGATGGTGA AATCGATCGC CGCAGGTCTG	60
ACCGCCGCGG CTGCAATCGG CGCCGCTGCG GCCGGTGTGA CTTGATCAT GGCTGGCGGN	120
CCGGTCGTAT ACCAGATGCA GCCGGTCGTC TTCGGCGCGC CACTGCCGTT GGACCCGGNA	180
TCCGCCCTG ANGTCCCGAC CGCCGCCAG TGGACCAGNC TGCTCAACAG NCTCGNCGAT	240
CCCAACGTGT CGTTTNGNAA CAAGGGNAGT CTGGTCGAGG GNGGNATCGG NGGNANCGAG	300
GGNGNGNATC GNCGANCA A	321

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT TCCGGTTGGC GACGGGTTTT GGGNGCGGGT GGTTAACCCG CTCGGCCAGC	60
CGATCGACGG GCGCGGAGAC GTCGACTCCG ATACTCGGCG CGCGCTGGAG CTCCAGGCGC	120
CCTCGGTGGT GNACCGGCAA GCGTGAAAGG AGCCGTTGNA GACCGGGATC AAGGCGATTG	180
ACGCGATGAC CCCGATCGGC CGCGGGCAGC GCCAGCTGAT CATCGGGGAC CGCAAGACCG	240
GCAAAAACCG CCGTCTGTGT CGGACACCAT CCTCAAACCA GCGGGAAGAA CTGGGAGTCC	300
GGTGGATCCC AAGAAGCAGG TGCCTTGTG TATACGTTGG CCATCGGGCA AGAAGGGGAA	360
CTTACCATCG CCG	373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGCCGT GATGGGATTC CTGGGCGGGG CCGGTCCGCT GGCGGTGGTG GATCAGCAAC	60
TGGTTACCCG GGTGCCGCAA GGCTGGTCGT TTGCTCAGGC AGCCGCTGTG CCGGTGGTGT	120
TCTTGACGGC CTGGTACGGG TTGGCCGATT TAGCCGAGAT CAAGGCGGGC GAATCGGTGC	180
TGATCCATGC CCGTACCGGC GGTGTGGGCA TGGCGGCTGT GCAGCTGGCT CGCCAGTGGG	240
GCGTGGAGGT TTTCGTCACC GCCAGCCGTG GNAAGTGGGA CACGCTGCGC GCCATNGNGT	300
TTGACGACGA NCCATATCGG NGATTCCNC ACATNCGAAG TTCCGANGGA GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGCG	TTCATTCCGT	TCGACCAGCG	GCTGGCGATA	ATCGACGAAG	TGATCAAGCC	60
GCGGTTTCGCG	GCGCTCATGG	GTCACAGCGA	GTAATCAGCA	AGTTCTCTGG	TATATCGCAC	120
CTAGCGTCCA	GTTGCTTGCC	AGATCGCTTT	CGTACCGTCA	TCGCATGTAC	CGGTTTCGCGT	180
GCCGCACGCT	CATGCTGGCG	GCGTGCATCC	TGGCCACGGG	TGTGGCGGGT	CTCGGGGTCG	240

GCGCGCAGTC CGCAGCCCAA ACCGCGCCGG TGCCCGACTA CTA CTGGTGC CCGGGGCAGC 300
 CTTTCGACCC CGCATGGGGG CCCAACTGGG ATCCCTACAC CTGCCATGAC GACTTCCACC 360
 GCGACAGCGA CGGCCCCGAC CACAGCCGCG ACTACCCCGG ACCCATCCTC GAAGGTCCCG 420
 TGCTTGACGA TCCCGGTGCT GCGCCGCCGC CCCC GGCTGC CGGTGGCGGC GCATAGCGCT 480
 CGTTGACCGG GCCGCATCAG CGAATACGCG TATAAACCCG GCGTGCCCC CGGCAAGCTA 540
 CGACCCCGG CGGGGCAGAT TTACGCTCCC GTGCCGATGG ATCGCGCCGT CCGATGACAG 600
 AAAATAGGCG ACGGTTTTGG CAACCGCTTG GAGGACGCTT GAAGGGAACC TGTCATGAAC 660
 GGCGACAGCG CCTCCACCAT CGACATCGAC AAGGTTGTTA CCCGCACACC CGTTCGCCGG 720
 ATCGTG 726

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACG ACGAACGTCG GGCCCACCAC CGCCTATGCG TTGATGCAGG CGACCGGGAT 60
 GGTGCGCGAC CATATCCAAG CATGCTGGGT GCCCACTGAG CGACCTTTTG ACCAGCCGGG 120
 CTGCCCCGATG GCGGCCCCGGT GAAGTCATTG CGCCGGGGCT TGTGCACCTG ATGAACCCGA 180
 ATAGGGAACA ATAGGGGGGT GATTTGGCAG TTCAATGTCG GGTATGGCTG GAAATCCAAT 240
 GGCGGGGCAT GCTCGGCGCC GACCAGGCTC GCGCAGGCGG GCCAGCCCGA ATCTGGAGGG 300
 AGCACTCAAT GCGGCGGATG AAGCCCCGGA CCGGCGACGG TCCTTTGGAA GCAACTAAGG 360

AGGGGCGCGG CATTGTGATG CGAGTACCAC TTGAGGGTGG CGGTCGCCTG GTCGTCGAGC	420
TGACACCCGA CGAAGCCGCC GCACTGGGTG ACGAACTCAA AGGCGTTACT AGCTAAGACC	480
AGCCCAACGG CGAATGGTCG GCGTTACGCG CACACCTTCC GGTAGATGTC CAGTGTCTGC	540
TCGGCGATGT ATGCCAGGA GAACTCTTGG ATACAGCGCT	580

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCG CCGGGGGTTT TGGCGGGGCC GGGGCGGTG GCGGCAACGG CGGGGCCGGC	60
GGTACCGCCG GGTGTTCGG TGTCGGCGGG GCCGGTGGGG CCGGAGGCAA CGGCATCGCC	120
GGTGTCACGG GTACGTCGGC CAGCACACCG GGTGGATCCG	160

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA CGATGGTGAT GTACGCCAAC GTTGTGACA CGCTCGAGGC GTTCACGATC	60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGCCC CGTTCGCGGA GGCGGCTGCC	120

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(2) INFORMATION FOR SEQ ID NO:28:

(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

GCAGCCGGTG GTTCTCGGAC TATCTGCGCA CGGTGACGCA GCGCGACGTG CGCGAGCTGA	60
AGCGGATCGA GCAGACGGAT CGCCTGCCGC GGTTTCATGCG CTACCTGGCC GCTATCACCG	120
CGCAGGAGCT GAACGTGGCC GAAGCGGCGC GGGTCATCGG GGTCGACGCG GGGACGATCC	180
GTTTCGGATCT GGCCTGGTTC GAGACGGTCT ATCTGGTACA TCGCCTGCCC GCCTGGTCGC	240
GGAATCTGAC CGCGAAGATC AAGAAGCGGT CAAAGATCCA CGTCGTCGAC AGTGGCTTCG	300
CGGCCTGGTT GCGCGGG	317

(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG CTGTCGATGA ACAGCGTTGC CGGACGCGCG GCGGCCAGCA CGTCGGTGTA	60
GCAGCGCCGG ACCACCTCGC CGGTGGGCAG CATGGTGATG ACCACGTCGG CCTCGGCCAC	120
C&CTTCGGGC GCGCTACGAA ACACCGCGAC ACCGTGCGCG GCGGCGCCGG ACGCCGCCGT	180
GG	182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG	TTTGGTGAGC	AGGTGGTCGA	CGCGAAAGTC	TGGGCGCCTG	CGAAGCGGGT	60
CGGCGTTCAC	GAGGCGAAGA	CACGCCTGTC	CGAGCTGCTG	CGGCTCGTCT	ACGGCGGGCA	120
GAGGTTGAGA	TTGCCC GCCG	CGGCGAGCCG	G TAGCAAAGC	TTGTGCCGCT	GCATCCTCAT	180
GAGACTCGGC	GGTTAGGCAT	TGACCATGGC	GTGTACCGCG	TGCCCGACGA	TTTGGACGCT	240
CCGTTGTCAG	ACGACGTGCT	CGAACGCTTT	CACCGGTGAA	GCGCTACCTC	ATCGACACCC	300
ACGTTTGG						308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA	GCAACTCACG	TGGATGATGG	TCGGCAGCGG	CATTGAGGAC	GGAGAGAATC	60
CGGCCGAAGC	TGCCGCGCGG	CAAGTGCTCA	TAGTGACCGG	CCGTAGAGGG	CTCCCCGAT	120
GGCACC GGAC	TATTCTGGTG	TGCCGCTGGC	CGGTAAGAGC	GGGTAAAAGA	ATGTGAGGGG	180
ACACGATGAG	CAATCACACC	TACCGAGTGA	TCGAGATCGT	CGGGACCTCG	CCCGACGGCG	240
TCGACGCGGC	AATCCAGGGC	GGTCTGG				267

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGCCGA	AAGAATGTGA	GGGGACACGA	TGAGCAATCA	CACCTACCGA	GTGATCGAGA	60
TCGTCTGGGAC	CTCGCCCGAC	GGCGTCGACG	CGGCAATCCA	GGGCGGTCTG	GCCCGAGCTG	120
CGCAGACCAT	GCGCGCGCTG	GACTGGTTCG	AAGTACAGTC	AATTCGAGGC	CACCTGGTCG	180
ACGGAGCGGT	CGCGCACTTC	CAGGTGACTA	TGAAAGTCGG	CTTCCGCTGG	AGGATTCCTG	240
AACCTTCAAG	CGCGGCCGAT	AACTGAGGTG	CATCATTAAG	CGACTTTTCC	AGAACATCCT	300
GACGCGCTCG	AAACGCGGTT	CAGCCGACGG	TGGCTCCGCC	GAGGCGCTGC	CTCCAAAATC	360
CCTGCGACAA	TTCGTCTGGCG	GCGCCTACAA	GGAAGTCGGT	GCTGAATTCG	TCGGGTATCT	420
GGTCGACCTG	TGTGGGCTGC	AGCCGGACGA	AGCGGTGCTC	GACGTCGGCT	GCGGCTCGGG	480
GCGGATGGCG	TTGCCGCTCA	CCGGCTATCT	GAACAGCGAG	GGACGCTACG	CCGGCTTCGA	540

TATCTCGCAG AAAGCCATCG CGTGGTGCCA GGAGCACATC ACCTCGGCGC ACCCCAAC TT 600
 CCAGTTCGAG GTCTCCGACA TCTACAAC TC GCTGTACAAC CCGAAAGGGA AATACCAGTC 660
 ACTAGACTTT CGCTTTCCAT ATCCGGATGC GTCGTTGAT GTGGTGTTTC TTACCTCGGT 720
 GTTCACCCAC ATGTTTCCGC CGGACGTGGA GCACTATCTG GACGAGATCT CCCGCGTGCT 780
 GAAGCCCGGC GGACGATGCC TGTGCACGTA CTTCTTGCTC AATGACGAGT CGTTAGCCCA 840
 CATCGCGGAA GGAAAGAGTG CGCACAACTT CCAGCATGAG GGACCGGGTT ATCGGACAAT 900
 CCACAAGAAG CGGCCCCAAG AAGCAATCGG CTTGCCGGAG ACCTTCGTCA GGGATGTCTA 960
 TGGCAAGTTC GGCCTCGCCG TGCACGAACC ATTGCACTAC GGCTCATGGA GTGGCCGGGA 1020
 ACCACGCCTA AGCTTCCAGG ACATCGTCAT CGCGACCAAA ACCGCGAGCT AGGTCGGCAT 1080
 CCGGGAAGCA TCGCGACACC GTGGCGCCGA GCGCCGCTGC CGGCAGGCCG ATTAGGCGGG 1140
 CAGATTAGCC CGCCGCGGCT CCCGGCTCCG AGTACGGCGC CCCGAATGGC GTCACCGGCT 1200
 GGTAACCACG CTTGCGCGCC TGGGCGGGCG CCTGCCGGAT CAGGTGGTAG ATGCCGACAA 1260
 AGCCTGCGTG ATCGGTCATC ACCAACGGTG ACAGCAGCCG GTTGTGCACC AGCGCGAACG 1320
 CCACCCCGGT CTCCGGGTCT GTCCAGCCGA TCGAGCCGCC CAAGCCCACA TGACCAAACC 1380
 CCGGCATCAC GTTGCCGATC GGCATACCGT GATAGCCAAG ATGAAAATTT AAGGGCACCA 1440
 ATAGATTTTCG ATCCGGCAGA ACTTGCCGTC GGTTGCGGGT CAGGCCCGTG ACCAGCTCCC 1500
 GCGACAAGAA CCGTATGCCG TCGATCTCGC CTCGTGCCG 1539

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG GCGTGGATGA GCGTCACCGC GGGGCAGGCC GAGCTGACCG CCGCCCAGGT 60
 CCGGGTTGCT GCGGCGGCCT ACGAGACGGC GTATGGGCTG ACGGTGCCCC CGCCGGTGAT 120
 CGCCGAGAAC CGTGCTGAAC TGATGATTCT GATAGCGACC AACCTCTTGG GGCAAAACAC 180
 CCCGGCGATC GCGGTCAACG AGGCCGAATA CGGCGAGATG TGGGCCCAAG ACGCCGCCGC 240
 GATGTTTGGC TACGCCGCGG CGACGGCGAC GGCGACGGCG ACGTTGCTGC CGTTCGAGGA 300
 GGCGCCGGAG ATGACCAGCG CGGGTGGGCT CCTCGAGCAG GCCGCCGCGG TCGAGGAGGC 360
 CTCCGACACC GCCGCGGCGA ACCAGTTGAT GAACAATGTG CCCCAGGCGC TGAAACAGTT 420
 GGCCCAGCCC ACGCAGGGCA CCACGCCTTC TTCCAAGCTG GGTGGCCTGT GGAAGACGGT 480
 CTCGCCGCAT CGGTCGCCGA TCAGCAACAT GGTGTCGATG GCCAACAACC ACATGTCGAT 540
 GACCAACTCG GGTGTGTCGA TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTCC 600
 GGCGGCGGCC GCCCAGGCCG TGCAAACCGC GGCGCAAAAC GGGGTCCGGG CGATGAGCTC 660
 GCTGGGCAGC TCGCTGGGTT CTTGCGGTCT GGGCGGTGGG GTGGCCGCCA ACTTGGGTCG 720
 GGCGGCCTCG GTACGGTATG GTCACCGGGA TGGCGGAAAA TATGCANAGT CTGGTCGGCG 780
 GAACGGTGGT CCGGCGTAAG GTTTACCCCC GTTTTCTGGA TGCGGTGAAC TTCGTCAACG 840
 GAAACAGTTA C 851

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG GCGGAAATTT GGACCAGATT CGCCTCCGGC GATAACCCAA TCAATCGAAC	60
CTAGATTTAT TCCGTCCAGG GGCCCGAGTA ATGGCTCGCA GGAGAGGAAC CTTACTGCTG	120
CGGGCACCTG TCGTAGGTCC TCGATACGGC GGAAGGCGTC GACATTTTCC ACCGACACCC	180
CCATCCAAAC GTTCGAGGGC CACTCCAGCT TGTGAGCGAG GCGACGCAGT CGCAGGCTGC	240
GCTTGGTCAA GATC	254

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC	GAAGCGGCCG	CCGCCAAGGC	GAAGTCGCTG	TTGGACCAGG	AGGGACGGGA	60
CGATCTGGCG	CTGCGGATCG	CGGTTCA GCC	GGGGGGGTGC	GCTGGATTGC	GCTATAACCT	120
TTTCTTCGAC	GACCGGACGC	TGGATGGTGA	CCAAACCGCG	GAGTTCGGTG	GTGTCAGGTT	180
GATCGTGGAC	CGGATGAGCG	CGCCGTATGT	GGAAGGCGCG	TCGATCGATT	TCGTCGACAC	240
TATTGAGAAG	CAAGGTTTAC	CATCGACAAT	CCCAACGCCA	CCGGCTCCTG	CGCGTGCGGG	300
GATTCGTTCA	ACTGATAAAA	CGCTAGTACG	ACCCCGCGGT	GCGCAACACG	TACGAGCACA	360
CCAAGACCTG	ACCGCGCTGG	AAAAGCAACT	GAGCGATGCC	TTGCACCTGA	CCGCGTGGCG	420
GGCCGCCGGC	GGCAGGTGTC	ACCTGCATGG	TGAACAGCAC	CTGGGCCTGA	TATTGCGACC	480
AGTACACGAT	TTTGTCGATC	GAGGTCACTT	CGACCTGGGA	GAAGTGCTTG	CGGAACGCGT	540

CGCTGCTCAG CTTGGCCAAG GCCTGATCGG AGCGCTTGTC GCGCACGCCG TCGTGGATAC 600
 CGCACAGCGC ATTGCGAAG ATGGTGTCCA CATCGCGGTT CTCCAGCGCG TTGAGGTATC 660
 CCTGAATCGC GGTTTTGGCC GGTCCCTCCG AGAATGTGCC TGCCGTGTTG GCTCCGTTGG 720
 T^{*}GCGGACCCC GTATATGATC GCCGCCGTCA TAGCCGACAC CAGCGCGAGG GCTACCACAA 780
 TGCCGATCAG CAGCCGCTTG TGCCGTCGCT TCGGGTAGGA CACCTGCGGC GGCACGCCGG 840
 GATATGCGGC GGGCGGCAGC GCCGCGTCGT CTGCCGGTCC CGGGGCGAAG GCCGGTTCGG 900
 CGGCGCCGAG GTCGTGGGGG TAGTCCAGGG CTTGGGGTTC GTGGGATGAG GGCTCGGGGT 960
 ACGGCGCCGG TCCGTTGGTG CCGACACCGG GGTTCGGCGA GTGGGGACCG GGCATTGTGG 1020
 TTCTCCTAGG GTGGTGGACG GGACCAGCTG CTAGGGCGAC AACCGCCCGT CGCGTCAGCC 1080
 GGCAGCATCG GCAATCAGGT GAGCTCCCTA GGCAGGCTAG CGCAACAGCT GCCGTCAGCT 1140
 CTC AACGCGA CGGGGCGGGC CGCGGCGCCG ATAATGTTGA AAGACTAGGC AACCTTAGGA 1200
 ACGAAGGACG GAGATTTTGT GACGATC 1227

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGGTGTCGG CGGATCCGGC GGGTGGTTGA ACGGCAACGG CGGGGCCGGC GGGGCCGGCG 60
 GGACCGGCGC TAACGGTGGT GCCGGCGGCA ACGCCTGGTT GTTCGGGGCC GGCGGGTCCG 120
 GCGGNGCCGG CACCAATGGT GGNGTCGGCG GGTCCGGCGG ATTTGTCTAC GGCAACGGCG 180
 G 181

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

GCGGTGTCGG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGTGTCGGC	GGCCGGGGCG	60
GCGACGGCGT	CTTTGCCGGT	GCCGGCGGCC	AGGGCGGCCT	CGGTGGGCAG	GGCGGCAATG	120
GCGGCGGCTC	CACCGGCGGC	AACGGCGGTC	TTGGCGGCGC	GGGCGGTGGC	GGAGGCAACG	180
CCCCGGACGG	CGGCTTCGGT	GGCAACGGCG	GTAAGGGTGG	CCAGGGCGGN	ATTGGCGGCG	240
GCACTCAGAG	CGCGACCGGC	CTCGNGGTG	ACGGCGGTGA	CGGCGGTGAC		290

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

GATCCAGTGG CATGGNGGGT GTCAGTGGAA GCAT 34

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

(2) INFORMATION FOR SEQ ID NO:40:

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:40:

(2) INFORMATION FOR SEQ ID NO:41:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

(2) INFORMATION FOR SEQ ID NO:42:

(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:43:

(A) LENGTH: 702 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCACC 60

CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTTCG CGATGCCGGC 120

ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT 180
 AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG 240
 AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC 300
 CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG 360
 CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT 420
 CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG 480
 ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCGTCGGA GGGGACAGTT 540
 CGGCCGAACT AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC 600
 TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG 660
 GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG 702

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCCGCAG CGCTGTCGGG CGACGTGGCG GTCAAAGCGG CATCGCTCGG TGGCGGTGGA 60
 GGCGGCGGGG TGCCGTCGGC GCCGTTGGGA TCCGCGATCG GGGGCGCCGA ATCGGTGCGG 120
 CCCGCTGGCG CTGGTGACAT TGCCGGCTTA GGCCAGGGAA GGGCCGGCGG CGGCGCCGCG 180
 CTGGGCGGCG GTGGCATGGG AATGCCGATG GGTGCCGCGC ATCAGGGACA AGGGGGCGCC 240
 AAGTCCAAGG GTTCTCAGCA GGAAGACGAG GCGCTCTACA CCGAGGATCC TCGTGCCG 298

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1058 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG	ATCGAATCGC	GTGCCCGGGA	GCACAGCGTC	GCACTGCACC	AGTGGAGGAG	60
CCATGACCTA	CTCGCCGGGT	AACCCCGGAT	ACCCGCAAGC	GCAGCCCGCA	GGCTCCTACG	120
GAGGCGTCAC	ACCCTCGTTC	GCCCACGCCG	ATGAGGGTGC	GAGCAAGCTA	CCGATGTACC	180
TGAACATCGC	GGTGGCAGTG	CTCGGTCTGG	CTGCGTACTT	CGCCAGCTTC	GGCCCAATGT	240
TCACCCTCAG	TACCGAACTC	GGGGGGGGTG	ATGGCGCAGT	GTCCGGTGAC	ACTGGGCTGC	300
CGGTCCGGGT	GGCTCTGCTG	GCTGCGCTGC	TTGCCGGGGT	GGTTCTGGTG	CCTAAGGCCA	360
AGAGCCATGT	GACGGTAGTT	GCGGTGCTCG	GGGTACTCGG	CGTATTTCTG	ATGGTCTCGG	420
CGACGTTTAA	CAAGCCCAGC	GCCTATTCGA	CCGTTTGGGC	ATTGTGGGTT	GTGTTGGCTT	480
TCATCGTGTT	CCAGGCGGTT	GCGGCAGTCC	TGGCGCTCTT	GGTGGAGACC	GGCGCTATCA	540
CCGCGCCGGC	GCCGCGGCCC	AAGTTCGACC	CGTATGGACA	GTACGGGCGG	TACGGGCAGT	600
ACGGGCAGTA	CGGGGTGCAG	CCGGGTGGGT	ACTACGGTCA	GCAGGGTGCT	CAGCAGGCCG	660
CGGGACTGCA	GTCGCCCCGC	CCGCAGCAGT	CTCCGCAGCC	TCCCGGATAT	GGGTCGCAGT	720
ACGGCGGCTA	TTCGTCCAGT	CCGAGCCAAT	CGGGCAGTGG	ATACACTGCT	CAGCCCCCGG	780
CCCAGCCGCC	GGCGCAGTCC	GGGTCGCAAC	AATCGCACCA	GGGCCCATCC	ACGCCACCTA	840
CCGGCTTTCC	GAGCTTCAGC	CCACCACCAC	CGGTCAGTGC	CGGGACGGGG	TCGCAGGCTG	900
GTTCGGCTCC	AGTCAACTAT	TCAAACCCCA	GCGGGGGCGA	GCAGTCGTCG	TCCCCCGGGG	960

GGGTGTCAGC AAGCGCGGAC GATCCTCGTG CCGAATTC 1058

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

CGGCACGAGA	GACCGATGCC	GCTACCCTCG	CGCAGGAGGC	AGGTAATTTT	GAGCGGATCT	60
CCGGCGACCT	GAAAACCCAG	ATCGACCAGG	TGGAGTCGAC	GGCAGGTTCT	TTGCAGGGCC	120
AGTGGCGCGG	CGCGGCGGGG	ACGGCCGCCC	AGGCCGCGGT	GGTGCCTTCT	CAAGAAGCAG	180
CCAATAAGCA	GAAGCAGGAA	CTCGACGAGA	TCTCGACGAA	TATTCGTCAG	GCCGGCGTCC	240
AATACTCGAG	GGCCGACGAG	GAGCAGCAGC	AGGCGCTGTC	CTCGCAAATG	GGCTTCTGAC	300
CCGCTAATAC	GAAAAGAAAC	GGAGCAA				327

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

CGGTCGCGAT GATGGCGTTG TCGAACGTGA CCGATTCTGT ACCGCCGTG T TGAGATCAA 60

CCAACAACGT GTTGGCGTCG GCAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTTCT 120

TCTTCATCAG GAAGTGCACA CCGGCCACCC TGCCCTCGGN TACCTTTCGG 170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGG CACGGGGGGT GCCGGCGGCA GCACCGCTGG CGCTGGCGGC AACGGCGGGG 60

CCGGGGGTGG CGGCGGAACC GGTGGGTTGC TCTTCGGCAA CGGCGGTGCC GGCGGGCACG 120

GGGCCGT 127

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGCGGCAAG GGCGGCACCG CCGGCAACGG GAGCGGCGCG GCCGGCGGCA ACGGCGGCAA 60

CGGCGGCTCC GGCCTCAACG G 81

(2) INFORMATION FOR SEQ ID NO:50:

09724689-42800

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCCGGCTCC GGCCAGAAGG GCGGTAACGG AGGAGCTGCC GGATTGTTTG 60
 GCAACGGCGG GGCCGGNGGT GCCGGCGCGT CCAACCAAGC CGGTAACGGC GGNGCCGGCG 120
 GAAACGGTGG TGCCGGTGGG CTGATCTGG 149

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA TCACACCTAC CGAGTGATCG AGATCGTCGG GACCTCGCCC GACGGTGTCTG 60
 ACGCGGNAAT CCAGGGCGGT CTGGCCCGAG CTGCGCAGAC CATGCGCGCG CTGGACTGGT 120
 TCGAAGTACA GTCAATTCGA GGCCACCTGG TCGACGGAGC GGTCGCGCAC TTCCAGGTGA 180
 CTATGAAAGT CGGCTTCCGC CTGGAGGATT CCTGAACCTT CAAGCGCGGC CGATAACTGA 240
 GGTGCATCAT TAAGCGACTT TTCCAGAACA TCCTGACGCG CTCGAAACGC GGTTCAGCCG 300
 ACGGTGGCTC CGCCGAGGCG CTGCCTCCAA AATCCCTGCG ACAATTCGTC GGCGG 355

(2) INFORMATION FOR SEQ ID NO:52:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA	60
CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG	120
CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCCTCG	180
CCGCCGTGCA CCGCTGCAGC GCCACCCGCA CCGGCGACAC CTGTTGCCCC CCCACCACCG	240
GCCGCCGCCA ACACGCCGAA TGCCAGCCG GCGATCCCA ACGCAGCACC TCCGCCGGCC	300
GACCCGAACG CACCGCCGCC ACCTGTCATT GCCCCAAACG CACCCCAACC TGTCCGGATC	360
GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC	420
GCCCACTTCG ACTACGGTTC AGCACTCTC AGCAAAACCA CCGGGGACCC GCCATTTCCC	480
GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAG	540
CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG	600
GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC	660
GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG	720
CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGGCGAACGC ACCGGACGCC	780
GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG	840
GGCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCCGGCGCCG	900
GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCCG CCGGGGAAGT CGCTCCTACC	960

CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCCTGA

999

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1 5 10 15
 Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
 20 25 30
 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 45
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 50 55 60
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 65 70 75 80
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 85 90 95
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
 100 105 110
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 115 120 125
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 130 135 140
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 145 150 155 160

CCGACGACACCGCA

(2) INFORMATION FOR SEQ ID NO:54:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

• Val Ala Ala Leu
20

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
1 5 10 15

(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

0972463W 112000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala	Glu	Glu	Ser	Ile	Ser	Thr	Xaa	Glu	Xaa	Ile	Val	Pro
1				5					10			

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp	Pro	Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Ala	Ala	Ala	Ala	Pro	Pro
1				5				10						15	

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala	Pro	Lys	Thr	Tyr	Xaa	Glu	Glu	Leu	Lys	Gly	Thr	Asp	Thr	Gly
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:62:

0972463W 442000

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
 1 5 10 15
 Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
 1 5 10 15
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
 20 25 30
 Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35 40 45
 Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
 50 55 60

09724633-443000

Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
180 185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg

(2) INFORMATION FOR SEQ ID NO:65:

(A) LENGTH: 230 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1 5 10 15

Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
20 25 30

Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO:66:

(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:71:

(A) LENGTH: 267 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:72:

(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1 5 10 15

Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
20 25 30

Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
35 40 45

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
50 55 60

Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
65 70 75 80

Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
85 90 95

Gln

(2) INFORMATION FOR SEQ ID NO:73:

(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala ...
1 5 10 15

Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
20 25 30

Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
35 40 45

Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
50 55 60

Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
65 70 75 80

Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
85 90 95

Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
100 105 110

Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
115 120 125

Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
130 135 140

Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
145 150 155 160

Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
165 170 175

Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
180 185 190

Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
195 200 205

Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
210 215 220

Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
225 230 235 240

Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
245 250 255

Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
260 265 270

Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
275 280 285

Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile
290 295 300

Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
305 310 315 320

Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
325 330 335

Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
340 345 350

Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
355 360

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

00724683 112800

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
1 5 10 15

Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
20 25 30

Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
35 40 45

Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
50 55 60

Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
65 70 75 80

Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
85 90 95

Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
100 105 110

Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
115 120 125

Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
130 135 140

Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
145 150 155 160

Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
165 170 175

Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
180 185 190

Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
195 200 205

Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg

220

Asn Arg Pro Arg Arg
305

(A) LENGTH: 580 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
50 55 60

Arg 65	Phe	Arg	Ser	Phe	Pro 70	Val	Arg	Arg	Leu	Ala 75	Leu	Gly	Ala	Arg	Thr 80
Ser	Arg	Thr	Leu	Gly 85	Val	Arg	Arg	Thr	Leu 90	Ser	Gln	Trp	Asn	Leu 95	Ser
Pro	Arg	Ala	Gln	Pro	Ser	Cys	Ala	Val 105	Thr	Val	Glu	Ser	His 110	Thr	His
Ala	Ser	Pro	Arg	Met	Ala	Lys	Leu	Ala 120	Arg	Val	Val	Gly	Leu	Val	Gln
Glu	Glu	Gln	Pro	Ser	Asp	Met 135	Thr	Asn	His	Pro	Arg	Tyr	Ser	Pro	Pro
Pro 145	Gln	Gln	Pro	Gly	Thr 150	Pro	Gly	Tyr	Ala	Gln 155	Gly	Gln	Gln	Gln	Thr 160
Tyr	Ser	Gln	Gln	Phe	Asp 165	Trp	Arg	Tyr	Pro	Pro	Ser	Pro	Pro	Pro	Gln 175
Pro	Thr	Gln	Tyr	Arg	Gln	Pro	Tyr	Glu 185	Ala	Leu	Gly	Gly	Thr 190	Arg	Pro
Gly	Leu	Ile	Pro	Gly	Val	Ile 200	Pro	Thr	Met	Thr	Pro	Pro	Pro	Gly	Met 205
Val	Arg	Gln	Arg	Pro	Arg	Ala 215	Gly	Met	Leu	Ala	Ile 220	Gly	Ala	Val	Thr
Ile 225	Ala	Val	Val	Ser	Ala 230	Gly	Ile	Gly	Gly	Ala 235	Ala	Ala	Ser	Leu	Val 240
Gly	Phe	Asn	Arg	Ala	Pro	Ala	Gly	Pro	Ser 250	Gly	Gly	Pro	Val	Ala 255	Ala
Ser	Ala	Ala	Pro	Ser	Ile	Pro	Ala	Ala 265	Asn	Met	Pro	Pro	Gly 270	Ser	Val
Glu	Gln	Val	Ala	Ala	Lys	Val	Val	Pro 280	Ser	Val	Val	Met	Leu	Glu	Thr
Asp 290	Leu	Gly	Arg	Gln	Ser	Glu 295	Glu	Gly	Ser	Gly	Ile	Ile	Leu	Ser	Ala

Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu
530 535 540

Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr
545 550 555 560

Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly
565 570 575

Lys Ala Glu Gln
580

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
1 5 10 15

Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
20 25 30

Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
35 40 45

Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
50 55 60

Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu
65 70 75 80

Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala
85 90 95

Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg
100 105 110

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Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
 115 120 125

Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
 130 135 140

Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
 145 150 155 160

Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
 165 170 175

Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
 180 185 190

Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
 195 200 205

Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
 210 215 220

Lys Trp Asn Glu Pro Val Asn Val Asp
 225 230

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
 1 5 10 15

Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
 20 25 30

Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile

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45

Pro Arg
65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
1 5 10 15

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
20 25 30

Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
35 40 45

Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
50 55 60

Ser Pro Pro Leu Pro
65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Met 1	Ser	Asn	Ser	Arg 5	Arg	Arg	Ser	Leu	Arg 10	Trp	Ser	Trp	Leu	Leu 15	Ser
Val	Leu	Ala	Ala	Val	Gly	Leu	Gly	Leu	Ala	Thr	Ala	Pro	Ala	Gln	Ala
			20					25					30		
Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe	Ala	Asp	Phe	Pro	Ala	Leu
		35					40					45			
Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln	Val	Ala	Pro	Gln	Val	Val
	50					55					60				
Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn	Ala	Val	Gly	Ala	Gly	Thr
65					70					75					80
Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val	Leu	Thr	Asn	Asn	His	Val
				85					90					95	
Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe	Ser	Val	Gly	Ser	Gly	Gln
			100					105					110		
Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp	Arg	Thr	Gln	Asp	Val	Ala
		115					120					125			
Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	Leu	Pro	Ser	Ala	Ala	Ile	Gly
	130					135					140				
Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	Val	Ala	Met	Gly	Asn	Ser	Gly
145					150					155					160
Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro	Gly	Arg	Val	Val	Ala	Leu
				165					170					175	
Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu	Thr	Gly	Ala	Glu	Glu	Thr
			180					185					190		
Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala	Ile	Gln	Pro	Gly	Asp	Ser
		195					200					205			

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
210 215 220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
225 230 235 240

Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
245 250 255

Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
260 265 270

Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
275 280 285

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
1 5 10 15

Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
20 25 30

Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg
35 40 45

Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg
50 55 60

Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro
65 70 75 80

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Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
165 170

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp

(2) INFORMATION FOR SEQ ID NO:84:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
1 5 10 15

Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
20 25 30

Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly
35 40 45

Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
50 55 60

Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
65 70 75 80

Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Glu
85 90 95

Glu Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr
100 105 110

Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val
 1 5 10 15
 Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala
 20 25 30
 Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu
 35 40 45
 Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala
 50 55 60
 Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp
 65 70 75 80
 Gly Val Glu Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu
 85 90 95
 Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa
 100 105 110
 Arg Ser Ser Xaa Gly
 115

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
 1 5 10 15
 Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
 20 25 30
 Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
 35 40 45
 Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
 50 55 60
 His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
 65 70 75 80
 Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
 85 90 95
 Pro Ala Ala Gly Gly Gly Ala
 100

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
 1 5 10 15

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85

90

95

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1           5           10           15

Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
          20           25           30

Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
          35           40           45

Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
          50           55           60

Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
          65           70           75           80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
          85           90           95

Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
          100          105          110

Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
          115          120          125

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
          130          135          140

Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
          145          150          155          160

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50		55		60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe				
65		70		75
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe				
	85		90	95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala				
	100		105	110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met				
	115		120	125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly				
	130		135	140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro				
	145		150	155
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met				
	165		170	175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met				
	180		185	190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala				
	195		200	205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly				
	210		215	220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala				
	225		230	235
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly				
	245		250	255
Arg Arg Asn Gly Gly Pro Ala				
	260			

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

09724633 442000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met	Thr	Tyr	Ser	Pro	Gly	Asn	Pro	Gly	Tyr	Pro	Gln	Ala	Gln	Pro	Ala
1				5					10						15
Gly	Ser	Tyr	Gly	Gly	Val	Thr	Pro	Ser	Phe	Ala	His	Ala	Asp	Glu	Gly
			20					25					30		
Ala	Ser	Lys	Leu	Pro	Met	Tyr	Leu	Asn	Ile	Ala	Val	Ala	Val	Leu	Gly
		35					40					45			
Leu	Ala	Ala	Tyr	Phe	Ala	Ser	Phe	Gly	Pro	Met	Phe	Thr	Leu	Ser	Thr
	50					55					60				
Glu	Leu	Gly	Gly	Gly	Asp	Gly	Ala	Val	Ser	Gly	Asp	Thr	Gly	Leu	Pro
65					70					75					80
Val	Gly	Val	Ala	Leu	Leu	Ala	Ala	Leu	Leu	Ala	Gly	Val	Val	Leu	Val
				85					90					95	
Pro	Lys	Ala	Lys	Ser	His	Val	Thr	Val	Val	Ala	Val	Leu	Gly	Val	Leu
			100					105					110		
Gly	Val	Phe	Leu	Met	Val	Ser	Ala	Thr	Phe	Asn	Lys	Pro	Ser	Ala	Tyr
		115					120					125			
Ser	Thr	Gly	Trp	Ala	Leu	Trp	Val	Val	Leu	Ala	Phe	Ile	Val	Phe	Gln
	130					135					140				
Ala	Val	Ala	Ala	Val	Leu	Ala	Leu	Leu	Val	Glu	Thr	Gly	Ala	Ile	Thr
145					150					155					160
Ala	Pro	Ala	Pro	Arg	Pro	Lys	Phe	Asp	Pro	Tyr	Gly	Gln	Tyr	Gly	Arg
				165					170					175	
Tyr	Gly	Gln	Tyr	Gly	Gln	Tyr	Gly	Val	Gln	Pro	Gly	Gly	Tyr	Tyr	Gly
			180					185					190		

Pro Ser Gly Gly Glu Gln Ser Ser Ser Pro Gly Gly Ala Pro Val
290 295 300

(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Gln	Val	Glu	Ser	Thr	Ala	Gly	Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly	Cys	Gly	Ser	Thr	Ala	Gly	Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly	Ala
1				5					10					15	

Ala	Gly	Thr	Ala	Ala	Gln	Ala	Ala	Val	Val	Arg
			20					25		

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

097246800 42000

Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Gly Cys Gly Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu

Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAGATGG	TGAAATCGAT	CGCCGCAGGT	CTGACCGCCG	CGGCTGCAAT	CGGCGCCGCT	60
GCGGCCGGTG	TGACTTCGAT	CATGGCTGGC	GGCCCGGTCT	TATACCAGAT	GCAGCCGGTC	120
GTCTTCGGCG	CGCCACTGCC	GTTGGACCCG	GCATCCGCCC	CTGACGTCCC	GACCGCCGCC	180
CAGTTGACCA	GCCTGCTCAA	CAGCCTCGCC	GATCCCAACG	TGTCGTTTGC	GAACAAGGGC	240
AGTCTGGTCG	AGGGCGGCAT	CGGGGGCACC	GAGGCGCGCA	TCGCCGACCA	CAAGCTGAAG	300
AAGGCCGCCG	AGCACGGGGA	TCTGCCGCTG	TCGTTCAGCG	TGACGAACAT	CCAGCCGGCG	360
GCCGCCGGTT	CGGCCACCGC	CGACGTTTCC	GTCTCGGGTC	CGAAGCTCTC	GTCGCCGGTC	420
ACGCAGAACG	TCACGTTCGT	GAATCAAGGC	GGCTGGATGC	TGTCACGCGC	ATCGGCGATG	480
GAGTTGCTGC	AGGCCGCAGG	GAAGTGA				507

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
 1 5 10 15
 Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
 20 25 30
 Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
 35 40 45
 Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 50 55 60
 Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
 65 70 75 80
 Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
 85 90 95
 His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe
 100 105 110
 Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp
 115 120 125
 Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val
 130 135 140
 Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met
 145 150 155 160
 Glu Leu Leu Gln Ala Ala Gly Asn
 165

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid

0974631143000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

(2) INFORMATION FOR SEQ ID NO:102:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala

143

20

25

30

Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35 40 45

Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50 55 60

Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65 70 75 80

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85 90 95

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA 60
AATGTCACGT CCATTCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA 120
GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC 154

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

00024600 143000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1 5 10 15
 Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
 20 25 30
 Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 35 40 45
 Glu Ala Tyr
 50

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGTCGCGCA CTTCCAGGTG ACTATGAAAG TCGGCTTCCG NCTGGAGGAT TCCTGAACCT 60
 TCAAGCGCGG CCGATAACTG AGGTGCATCA TTAAGCGACT TTTCCAGAAC ATCCTGACGC 120
 GCTCGAAACG CGGCACAGCC GACGGTGGCT CCGNCGAGGC GCTGNCTCCA AAATCCCTGA 180
 GACAATTCGN CGGGGGCGCC TACAAGGAAG TCGGTGCTGA ATTCGNCNG TATCTGGTCG 240
 ACCTGTGTGG TCTGNAGCCG GACGAAGCGG TGCTCGACGT CG 282

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

• (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT	60
GGCATACCCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC	120
TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA	180
TGAGGTGTCG GCGCTGACTG CGGCGCACTT CGCCGCACAT GCGGCGATGT ATCAGTCCGT	240
GAGCGCTCGG GCTGCTGCGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG	300
CTCGTATGCG GCCACTGAAG TCGCCAATGC GGCGGCGGCC AGCTAAGCCA GGAACAGTCG	360
GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGGG TTTCGGGGCG TTACCACCGG	420
AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC CTCGCTGGTG GCCGCGGCTC	480
AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC GTCGGCGTTT CAGTCGGTGG	540
TCTGGGGTCT GACGGTGGGG TCGTGGATAG GTTCGTGCGC GGGTCTGATG GTGGCGGCGG	600
CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA GGCCGAGCTG ACCGCCGCCC	660
AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG GCTGACGGTG CCCCCGCCGG	720
TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA	780
ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGCGA GATGTGGGCC CAAGACGCCG	840
CCGCGATGTT TGGCTACGCC GCGGCGACGG CGACGGCGAC GGCGACGTTG CTGCCGTTG	900
AGGAGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC GCGGTCGAGG	960
AGGCCTCCGA CACCGCCGCG GCGAACCAGT TGATGAACAA TGTGCCCCAG GCGCTGCAAC	1020
AGCTGGCCCA GCCACGCAG GGCACCACGC CTTCTTCCAA GCTGGGTGGC CTGTGGAAGA	1080
CGGTCTCGCC GCATCGGTG CCGATCAGCA ACATGGTGTC GATGGCCAAC AACCACATGT	1140

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CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGGCTTTG 1200
 CTCCGGCGGC GGCCGCCCAG GCCGTGCAAA CCGCGGCGCA AAACGGGGTC CGGGCGATGA 1260
 GCTCGCTGGG CAGCTCGCTG GGTTCCTCGG GTCTGGGCGG TGGGGTGGCC GCCAACTTGG 1320
 GTCGGGCGGC CTCGGTCGGT TCGTTGTCGG TGCCGCAGGC CTGGGCCGCG GCCAACCAGG 1380
 CAGTCACCCC GGCGGCGCGG GCGCTGCCGC TGACCAGCCT GACCAGCGCC GCGGAAAGAG 1440
 GGCCCGGGCA GATGCTGGGC GGGCTGCCGG TGGGGCAGAT GGGCGCCAGG GCCGGTGGTG 1500
 GGCTCAGTGG TGTGCTGCGT GTTCCGCCGC GACCCTATGT GATGCCGCAT TCTCCGGCGG 1560
 CCGGCTAGGA GAGGGGGCGC AGACTGTCGT TATTTGACCA GTGATCGGCG GTCTCGGTGT 1620
 TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG 1680
 GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTTATG ACGGATCCGC ACGCGATGCG 1740
 GGACATGGCG GGCCGTTTTG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGAT 1800
 GTGGGCGTCC GCGCAAAACA TTTCCGGTGC GGGCTGGAGT GGCATGGCCG AGGCGACCTC 1860
 GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGCTGCACGG 1920
 GGTGCGTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA 1980
 GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAAT ACTTTTACAA GCGAAGGAGA 2040
 ACAGGTTTGA TGACCATCAA CTATCAATTC GGGGATGTG ACGCTCACGG CGCCATGATC 2100
 CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTGCTGA TGTGTTGACC 2160
 GCGAGTGACT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTCAT TACCCAGTTG 2220
 GGCCGTA ACT TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT 2280
 GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGGC CTGACACCAG 2340
 GCCAAGGCCA GGGACGTGGT GTACGAGTGA AGTTCCTCGC GTGATCCTTC GGGTGGCAGT 2400
 CTAAGTGGTC AGTGCTGGGG TGTTGGTGGT TTGCTGCTTG GCGGGTTCTT CGGTGCTGGT 2460

CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCAGG TAGCGCCGTC CTCGATCCA 2520
 TTCGTCGTGT TGTTCCGGCA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCGGG 2580
 GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT 2640
 GJTGGACCAG ATTTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT 2700
 GCGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC 2760
 CCGATCATAT TGGGCAACAA CTGATTCGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG 2820
 GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG 2880
 GGTCTGCAG CGCTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCGG CCACCAGGCC 2940
 GGCCTGGGCG TCGCTGGTGA CCAGCGCGAC CCCGGACAGG CCGCGGGCGA CCAGGTCGCG 3000
 GAAGAACGCC AGCCAGCCGG CCCCCTCCTC GCGGAGGTG ACCTGGATGC CCAGGATC 3058

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met
1				5					10					15	
Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp
			20					25					30		
Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser
		35				40					45				
Val	Val	Trp	Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly
	50					55					60				

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Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	65	70	75	80
Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	85	90	95	
Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	100	105	110	
Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	115	120	125	
Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	130	135	140	
Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	145	150	155	160
Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	165	170	175	
Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	180	185	190	
Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	195	200	205	
Gln	Gln	Leu	Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	210	215	220	
Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	225	230	235	240
Met	Val	Ser	Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	245	250	255	
Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	260	265	270	
Ala	Ala	Ala	Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	275	280	285	
Met	Ser	Ser	Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	290	295	300	

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
370 375 380

Pro His Ser Pro Ala Ala Gly
385 390

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACGTCAGCA CCCGCCGTGC AGGGCTGGAG CGTGGTCGGT TTTGATCTGC GGTCAAGGTG	60
ACGTCCCTCG GCGTGTCGCC GGC GTGGATG CAGACTCGAT GCCGCTCTTT AGTGCAACTA	120
ATTTCGTTGA AGTGCCTGCG AGGTATAGGA CTTCACGATT GGTTAATGTA GCGTTCACCC	180
CGTGTTGGGG TCGATTTGGC CGGACCAGTC GTCACCAACG CTTGGCGTGC GCGCCAGGCG	240
GGCGATCAGA TCGCTTGACT ACCAATCAAT CTTGAGCTCC CGGGCCGATG CTCGGGCTAA	300
ATGAGGAGGA GCACGCGTGT CTTTCACTGC GCAACCGGAG ATGTTGGCGG CCGCGGCTGG	360

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CGAACTTCGT	TCCCTGGGGG	CAACGCTGAA	GGCTAGCAAT	GCCGCCGCAG	CCGTGCCGAC	420
GA	CTGCCCCCGG	CTGCCGACGA	GGTGTCGCTG	CTGCTTGCCA	CACAATTCCG	480
TACGCATGCG	GCGACGTATC	AGACGGCCAG	CGCCAAGGCC	GCGGTGATCC	ATGAGCAGTT	540
TGTGACCACG	CTGGCCACCA	GCGCTAGTTC	ATATGCGGAC	ACCGAGGCCG	CCAACGCTGT	600
GGTCACCGGC	TAGCTGACCT	GACGGTATTC	GAGCGGAAGG	ATTATCGAAG	TGGTGGATTT	660
CGGGGCGTTA	CCACCGGAGA	TCAACTCCGC	GAGGATGTAC	GCCGGCCCCG	GTTCCGGCCTC	720
GCTGGTGGCC	GCCGCGAAGA	TGTGGGACAG	CGTGGCGAGT	GACCTGTTTT	CGGCCGCGTC	780
GGCGTTTCAG	TCGGTGGTCT	GGGGTCTGAC	GGTGGGGTCG	TGGATAGGTT	CGTCGGCGGG	840
TCTGATGGCG	GCGGCGGCCT	CGCCGTATGT	GGCGTGGATG	AGCGTCACCG	CGGGGCAGGC	900
CCAGCTGACC	GCCGCCCAGG	TCCGGGTTGC	TGCGGCGGCC	TACGAGACAG	CGTATAGGCT	960
GACGGTGCCC	CCGCCGGTGA	TCGCCGAGAA	CCGTACCGAA	CTGATGACGC	TGACCGCGAC	1020
CAACCTCTTG	GGGCAAAACA	CGCCGGCGAT	CGAGGCCAAT	CAGGCCGCAT	ACAGCCAGAT	1080
GTGGGGCCAA	GACGCGGAGG	CGATGTATGG	CTACGCCGCC	ACGGCGGGCA	CGGCGACCGA	1140
GGCGTTGCTG	CCGTTTCGAGG	ACGCCCCACT	GATCACCAAC	CCCGGCGGGC	TCCTTGAGCA	1200
GGCCGTCGCG	GTCGAGGAGG	CCATCGACAC	CGCCGCGGCG	AACCAGTTGA	TGAACAATGT	1260
GCCCCAAGCG	CTGCAACAGC	TGGCCCAGCC	AGCGCAGGGC	GTCGTACCTT	CTTCCAAGCT	1320
GGGTGGGCTG	TGGACGGCGG	TCTCGCCGCA	TCTGTCGCCG	CTCAGCAACG	TCAGTTCGAT	1380
AGCCAACAAC	CACATGTCGA	TGATGGGCAC	GGGTGTGTCTG	ATGACCAACA	CCTTGCACTC	1440
GATGTTGAAG	GGCTTAGCTC	CGGCGGCGGC	TCAGGCCGTG	GAAACCGCGG	CGGAAAACGG	1500
GGTCTGGGCG	ATGAGCTCGC	TGGGCAGCCA	GCTGGGTTCG	TCGCTGGGTT	CTTCGGGTCT	1560
GGGCGCTGGG	GTGGCCGCCA	ACTTGGGTCG	GGCGGCCTCG	GTCGGTTCGT	TGTCGGTGCC	1620
GCCAGCATGG	GCCGCGGCCA	ACCAGGCGGT	CACCCCGGCG	GCGCGGGCGC	TGCCGCTGAC	1680
CAGCCTGACC	AGCGCCGCCC	AAACCGCCCC	CGGACACATG	CTGGG		1725

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1 5 10 15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20 25 30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35 40 45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
50 55 60

Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65 70 75 80

Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
85 90 95

Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
100 105 110

Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
115 120 125

Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
130 135 140

Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:110:

(A) LENGTH: 3027 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

ACGGGACAAT CGCGCTGTTG TGTATTCACC CGACACGTCG ACCAAGACTT CGCTACCGCC 1200
 AGGTGCGACC TCGCCGGCGA TTTCCTGTCC TATACGACCA GTTCACGCAG CAGATCGTGG 1260
 CTCCGGCGGC CAAACAGAAG TCACTGAAAA CCACCGCCAA GGTGGTGCGC GCGGCCGTGT 1320
 CGGAGCTACA TCCGGATTCG GCCGTCGTTT TGGTTTTTGT CGACCAGAGC ACTACCAGTA 1380
 AGGACAGCCC CAATCCGTCG ATGGCGGCCA GCAGCGTGAT GGTGACCCTA GCCAAGGTCG 1440
 ACGGCAATTG GCTGATCACC AAGTTCACCC CGGTTTAGGT TGCCGTAGGC GGTCGCCAAG 1500
 TCTGACGGGG GCGCGGGTGG CTGCTCGTGC GAGATACCGG CCGTTCTCCG GACAATCACG 1560
 GCCCGACCTC AAACAGATCT CGGCCGCTGT CTAATCGGCC GGGTTATTTA AGATTAGTTG 1620
 CCACTGTATT TACCTGATGT TCAGATTGTT CAGCTGGATT TAGCTTCGCG GCAGGGCGGC 1680
 TGGTGCACTT TGCATCTGGG GTTGTGACTA CTTGAGAGAA TTTGACCTGT TGCCGACGTT 1740
 GTTTGCTGTC CATCATTGGT GCTAGTTATG GCCGAGCGGA AGGATTATCG AAGTGGTGGA 1800
 CTTGCGGGCG TTACCACCGG AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC 1860
 CTCGCTGGTG GCCGCCGCGA AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC 1920
 GTCGGCGTTT CAGTCGGTGG TCTGGGTCT GACGACGGGA TCGTGGATAG GTTCGTCGGC 1980
 GGGTCTGATG GTGGCGGCGG CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA 2040
 GGCCGAGCTG ACCGCCGCC AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG 2100
 GCTGACGGTG CCCCCGCCG TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC 2160
 GACCAACCTC TTGGGGCAAA ACACCCGGC GATCGCGGTC AACGAGGCCG AATACGGGGA 2220
 GATGTGGGCC CAAGACGCCG CCGCGATGTT TGGCTACGCC GCCACGGCGG CGACGGCGAC 2280
 CGAGGCGTTG CTGCCGTTTG AGGACGCCCC ACTGATCACC AACCCGGCG GGCTCCTTGA 2340
 GCAGGCCGTC GCGGTCGAGG AGGCCATCGA CACCGCCGCG GCGAACCAGT TGATGAACAA 2400
 TGTGCCCCAA GCGCTGCAAC AACTGGCCCA GCCACGAAA AGCATCTGGC CGTTCGACCA 2460

ACTGAGTGAA CTCTGGAAAG CCATCTCGCC GCATCTGTCG CCGCTCAGCA ACATCGTGTC 2520
 GATGCTCAAC AACCACGTGT CGATGACCAA CTCGGGTGTG TCGATGGCCA GCACCTTGCA 2580
 CTCAATGTTG AAGGGCTTTG CTCCGGCGGC GGCTCAGGCC GTGGAAACCG CGGCGCAAAA 2640
 CGGGGTCCAG GCGATGAGCT CGCTGGGCAG CCAGCTGGGT TCGTCGCTGG GTTCTTCGGG 2700
 TCTGGGCGCT GGGGTGGCCG CCAACTTGGG TCGGGCGGCC TCGGTCGGTT CGTTGTCGGT 2760
 GCCGCAGGCC TGGGCCGCGG CCAACCAGGC GGTACCCCG GCGGCGCGGG CGCTGCCGCT 2820
 GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCCGACAC ATGCTGGGCG GGCTACCGCT 2880
 GGGGCAACTG ACCAATAGCG GCGGCGGGTT CGGCGGGGTT AGCAATGCGT TCGGGATGCC 2940
 GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCCGGG TAACGCCGAT CCGCACGCAA 3000
 TCGGGGCCCT CTATGCGGGC AGCGATC 3027

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met
1				5					10					15	
Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Lys	Met	Trp
			20					25					30		
Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser
		35					40					45			
Val	Val	Trp	Gly	Leu	Thr	Thr	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly
		50					55				60				

Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
305 310 315 320

Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
325 330 335

Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
340 345 350

Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn
355 360 365

Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro
370 375 380

Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly
385 390 395

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACC ATGCTGTGGC ACGCAATGCC ACCGGAGTAA ATACCGCACG	60
GCTGATGGCC GGCGCGGGTC CGGCTCCAAT GCTTGCGGCG GCCGCGGGAT GGCAGACGCT	120
TTCGGCGGCT CTGGACGCTC AGGCCGTCGA GTTGACCGCG CGCCTGAACT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGCT GCAACGCCGA TGGTGGTCTG	240
GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCGATG CAGGCGACGG CGCAAGCCGC	300
GGCATAACCC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATCGCCG CCAACCACAT	360

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260 265 270
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
 275 280 285
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
 290 295 300
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
 305 310 315 320
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
 325 330 335
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
 340 345 350
 Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp
 355 360 365

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
 1 5 10 15
 Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
 20 25 30
 Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
 35 40 45
 Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys

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50 55 60
 Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
 65 70 75 80
 Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
 85 90 95
 Gln Met Gly Phe
 100

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA	60
GGGCCAGTGG CGCGGCGCGG CGGGGACGGC CGCCCAGGCC GCGGTGGTGC GCTTCCAAGA	120
AGCAGCCAAT AAGCAGAAGC AGGAACTCGA CGAGATCTCG ACGAATATTC GTCAGGCCGG	180
CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCG CTGTCCTCGC AAATGGGCTT	240
CTGACCCGCT AATACGAAAA GAAACGGAGC AAAAACATGA CAGAGCAGCA GTGGAATTTC	300
GCGGGTATCG AGGCCGCGGC AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCCTC	360
CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA	396

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser
1				5				10						15	
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn		
				20				25					30		

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp	Pro	Pro	Asp	Pro	His	Gln	Xaa	Asp	Met	Thr	Lys	Gly	Tyr	Tyr	Pro
1				5				10						15	
Gly	Gly	Arg	Arg	Xaa	Phe										
				20											

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

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Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

00724635 112000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile
1 5 10 15

Asn Val His Leu Val
20

09724533-442000

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xj) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCAACGCTGT CGTGGCCTTT GCGGTGATCG GTTTCGCCTC GCTGGCGGTG GCGGTGGCGG 60
 TCACCATCCG ACCGACCGCG GCCTCAAAAC CGGTAGAGGG ACACCAAAAC GCCCAGCCAG 120
 GGAAGTTCAT GCCGTTGTTG CCGACGCAAC AGCAGGCGCC GGTCCCGCCG CCTCCGCCCG 180
 ATGATCCCAC CGCTGGATTC CAGGGCGGCA CCATTCCGGC TGTACAGAAC GTGGTGCCGC 240
 GGCCGGGTAC CTCACCCGGG GTGGGTGGGA CGCCGGCTTC GCCTGCGCCG GAAGCGCCGG 300
 CCGTGCCCGG TGTTGTGCCT GCCCCGGTGC CAATCCCGGT CCCGATCATC ATTCCCCCGT 360
 TCCCGGGTTG GCAGCCTGGA ATGCCGACCA TCCCACCGC ACCGCCGACG ACGCCGGTGA 420
 CCACGTCGGC GACGACGCCG CCGACCACGC CGCCGACCAC GCCGGTGACC ACGCCGCCAA 480
 CGACGCCGCC GACCACGCCG GTGACCACGC CGCCAACGAC GCCGCCGACC ACGCCGGTGA 540
 CCACGCCACC AACGACCGTC GCCCCGACGA CCGTCGCCCC GACGACGGTC GCTCCGACCA 600
 CCGTCGCCCC GACCACGGTC GCTCCAGCCA CCGCCACGCC GACGACCGTC GCTCCGCAGC 660
 CGACGCAGCA GCCCAGCAA CAACCAACCC AACAGATGCC AACCCAGCAG CAGACCGTGG 720
 CCCCAGAC GGTGGCGCCG GCTCCGCAGC CGCCGTCCGG TGGCCGAAC GGCAGCGGCG 780
 GGGGCGACTT ATTCGGCGGG TTCTGATCAC GGTCGCGGCT TCACTACGGT CGGAGGACAT 840
 GGCCGGTGAT GCGGTGACGG TGGTGCTGCC CTGTCTCAAC GA 882

09724635 148800

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 815 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA ACCGCTCGCG CCGCCCGCGC CGCCGGATCC GCCGTCGCCG CCACGCCCGC	60
CGGTGCCTCC GGTGCCCCCG TTGCCGCCGT CGCCGCCGTC GCCGCCGACC GGCTGGGTGC	120
CTAGGGCGCT GTTACCGCCC TGTTGGCGG GGACGCCGCC GGCACCACCG GTACCGCCGA	180
TGGCGCCGTT GCCGCCGGCG GCACCGTTGC CACCGTTGCC ACCGTTGCCA CCGTTGCCGA	240
CCAGCCACCC GCCGCGACCA CCGGCACCGC CGGCGCCGCC CGCACCGCCG GCGTGCCCGT	300
TCGTGCCCGT ACCGCCGGCA CCGCCGTTGC CGCCGTCACC GCCGACGGAA CTACCGGCGG	360
ACGCGGCCTG CCCGCCGGCG CCGCCCGCAC CGCCATTGGC ACCGCCGTCA CCGCCGGCTG	420
GGAGTGCCGC GATTAGGGCA CTGACCGGCG CAACCAGCGC AAGTACTCTC GGTCACCGAG	480
CACTTCCAGA CGACACCACA GCACGGGGTT GTCGGCGGAC TGGGTGAAAT GGCAGCCGAT	540
AGCGGCTAGC TGTCGGCTGC GGTCAACCTC GATCATGATG TCGAGGTGAC CGTGACCGCG	600
CCCCCGAAG GAGGCGCTGA ACTCGGCGTT GAGCCGATCG GCGATCGGTT GGGGCAGTGC	660
CCAGGCCAAT ACGGGGATAC CGGGTGTGNA AGCCGCCGCG AGCGCAGCTT CGGTTGCGCG	720
ACNGTGGTCG GGGTGGCCTG TTACGCCGTT GTCNTCGAAC ACGAGTAGCA GGTCTGCTCC	780
GGCGAGGGCA TCCACCACGC GTTGCCTCAG CTCGT	815

(2) INFORMATION FOR SEQ ID NO:140:

CCATCAACCA ACCGCTCGCG CCGCCCGCGC CGCCGGATCC GCCGTCGCCG CCACGCCCGC

CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC 1020
 ATACCGCCGG CAACTCACC GGCAGCGAAC AGGCCTGGCA CCGTGGCGGC GCCGGTGTCC 1080
 GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTGC GCCCGACTTC CATTGCCTGC 1140
 GTTCGGCACG AG 1152

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCCGCATGAG TGCCGACGAC 60
 CAGCAATGCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGGTCCA CGTGGGCGAT 120
 CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTTGGGCAGG GTCATCCGAC GTGTTTCCGC 180
 CGTGGTTTGC CGCATTATG CCGGCGCGCC GCGTCGGGCG GCCGGTATGG CCGAANGTCG 240
 ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTTGA GCGTCGCGCG GGGCAGCTTC 300
 GCCGGCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGCGG 360
 TGCAGCCCAC CCTCATTGGC GATGGCGCCG ACGATGGCGC CTGGACCGAT CTTGTGCCGC 420
 TTGCCGACGG CGACGCGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCCT TTGCGGACGG 480
 TCCCGACGCT GGTGCGGGTT GCGCCGCGAA AGCGGCGGGT CGGGTGCCAT CAGGAATGCC 540
 TCACCGCCGC GGCAGTGCAC GGCCAGTGCC GCGGCGATGT CAGCCATCGG GACATCATGC 600
 TCGCGTTCAT ACTCCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA 655

09741635 12300

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

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Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
1           5           10           15

Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu
20           25           30

Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
35           40           45

Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Pro Asp Asp Pro Thr Ala
50           55           60

Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
65           70           75           80

Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
85           90           95

Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
100          105          110

Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
115          120          125

Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
130          135          140

Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr
145          150          155          160

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0024000 12000

Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
 165 170 175

Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
 180 185 190

Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro
 195 200 205

Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro
 210 215 220

Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala
 225 230 235 240

Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn
 245 250 255

Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe
 260 265

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro
 1 5 10 15

Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro
 20 25 30

Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu
 35 40 45

09724633 " 412000

(2) INFORMATION FOR SEQ ID NO:144:

(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
1 5 10 15
Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
20 25 30

Asn Arg Arg
35

(2) INFORMATION FOR SEQ ID NO:145:

• (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
1 5 10 15

Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
20 25 30

Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
35 40 45

Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
50 55 60

Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
65 70 75 80

Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
85 90 95

Gly Gln Leu Arg Arg Gln Phe Tyr
100

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR primer"

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

- (2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR Primer"

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mycobacterium tuberculosis

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

- (2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PCR Primer"

054469-4800

(A) ORGANISM: *Mycobacterium tuberculosis*

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1993 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTTC TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC	220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC	268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG	316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly	
75 80 85	
TCT GGT GCC GGG ATC GCG CAG GCC GCC GCC GGG ACG GTC AAC ATT GGG	460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGG	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	
CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC	556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn	
120 125 130 135	
CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG	604
Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala	
140 145 150	
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT	652

Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala	
155 160 165	
GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG	700
Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu	
170 175 180	
CAC CGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG	748
His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu	
185 190 195	
TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC	796
Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr	
200 205 210 215	
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC	844
Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn	
220 225 230	
GGC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT	892
Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr	
235 240 245	
ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG	940
Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu	
250 255 260	
GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA	988
Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln	
265 270 275	
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC	1036
Ser Ile Gln Ala Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn	
280 285 290 295	
CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC	1084
Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile	
300 305 310	
ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GCC GCC	1132
Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala	
315 320 325	
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC	1180
Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly	

330	335	340	
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC			1228
Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC			1273
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAGCCTCGTT GACCACCACG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA			1333
GCATGCTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTGGGTG			1393
GGATAGGTGC GGTGATCCCG CTGCTTGCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG			1453
AGGCGATGGG TGCGATCAGG CTCAACGGGT TGCATTTCTT CACCGCCACC GAATGGAATC			1513
CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA			1573
CTACGGGGCG TTGCCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT			1633
CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT			1693
GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCCAGCG TGGTCGTCGG			1753
TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC			1813
TCACAACGCT CCCGATGTGC CGGTGCTGAA CTA CTGCGC GGCGACCCGG GCAACGGGGA			1873
GGGCATGTTG GTGTCCGGTC TGGTGTGGC GGTGATGGTC GTTCCCATTA TCGCCACCAC			1933
CACTCATGAC CTGTTCCGGC AGGTGCCGGT GTTGCCCCGG GAGGGCGCGA TCGGGAATTC			1993

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

09724635 428000

Val 1	Lys	Ile	Arg	Leu 5	His	Thr	Leu	Leu	Ala 10	Val	Leu	Thr	Ala	Ala 15	Pro
Leu	Leu	Leu	Ala 20	Ala	Ala	Gly	Cys	Gly 25	Ser	Lys	Pro	Pro	Ser	Gly	Ser
Pro	Glu	Thr 35	Gly	Ala	Gly	Ala	Gly 40	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser
Ser	Pro 50	Val	Thr	Leu	Ala	Glu 55	Thr	Gly	Ser	Thr	Leu 60	Leu	Tyr	Pro	Leu
Phe 65	Asn	Leu	Trp	Gly	Pro 70	Ala	Phe	His	Glu	Arg 75	Tyr	Pro	Asn	Val	Thr 80
Ile	Thr	Ala	Gln 85	Gly	Thr	Gly	Ser	Gly	Ala 90	Gly	Ile	Ala	Gln	Ala 95	Ala
Ala	Gly	Thr	Val 100	Asn	Ile	Gly	Ala	Ser	Asp 105	Ala	Tyr	Leu	Ser	Glu	Gly
Asp	Met	Ala	Ala	His	Lys	Gly 115	Leu	Met	Asn 120	Ile	Ala	Leu 125	Ala	Ile	Ser
Ala	Gln 130	Gln	Val	Asn	Tyr	Asn 135	Leu	Pro	Gly	Val	Ser 140	Glu	His	Leu	Lys
Leu 145	Asn	Gly	Lys	Val	Leu 150	Ala	Ala	Met	Tyr	Gln 155	Gly	Thr	Ile	Lys	Thr 160
Trp	Asp	Asp	Pro	Gln 165	Ile	Ala	Ala	Leu	Asn 170	Pro	Gly	Val	Asn	Leu 175	Pro
Gly	Thr	Ala	Val 180	Val	Pro	Leu	His	Arg 185	Ser	Asp	Gly	Ser	Gly	Asp	Thr
Phe	Leu	Phe 195	Thr	Gln	Tyr	Leu 200	Ser	Lys	Gln	Asp	Pro	Glu 205	Gly	Trp	Gly
Lys	Ser 210	Pro	Gly	Phe	Gly	Thr 215	Thr	Val	Asp	Phe	Pro	Ala 220	Val	Pro	Gly
Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys	Ala	Glu

225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

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 00024.594260